

# SEARCH REQUEST FORM

12-366

Requestor's  
Name: \_\_\_\_\_

Serial  
Number: \_\_\_\_\_

Date: \_\_\_\_\_

Phone: \_\_\_\_\_

Art Unit: \_\_\_\_\_

7E09

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 12-10-98

Searcher: POB x8-4291

Terminal time: 5

Elapsed time: prep 10

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: 6

### Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_\_ N.A. Sequence

1 A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

MP3 Other



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 MIPELH  
 \*\*\*\*\*  
 (TM)  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:15:56 1998; MasPar time 27.66 Seconds  
 547.553 Million cell updates/sec

Tabular output not generated.

Title: >US-08-455-970-12  
 Description: (1-936) from US08455970. pep  
 Perfect Score: 6217  
 Sequence: 1 MATVIDUSFPKTKAKIILY.....LSSIQFARGSHWSYGLRPG 936

Scoring table: PAM 150  
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-genes32  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26 27:part27 28:part28  
 29:part29

Statistics: Mean 37.888; Variance 222.402; scale 0.170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6217	100.0	977	19	W03942	LKT-GnRH protein fusi
2	6193	99.6	936	7	R34547	GnRH-leukotoxin gene
3	6135	98.7	1069	9	R52748	Bovine IFNgamma/LKT c
4	6135	98.7	1069	21	W13867	Chimeric protein #2.
5	6128	98.6	926	3	R14482	LKT352.
6	6128	98.6	926	7	R34545	Leukotoxin 352 produc
7	6128	98.6	926	10	R50291	Recombinant leukotoxi
8	6117	98.4	924	8	R42378	Recombinant leukotoxi
9	6117	98.4	924	8	R42380	Recombinant leukotoxi
10	6117	98.4	924	8	R42385	Recombinant leukotoxi
11	6119	98.4	926	19	W03945	P. haemolytica trunca
12	6107	98.2	943	7	R34546	Somatostatin-leukotox
13	6100	98.1	924	7	R34548	Rotavirus VP4-leukoto
14	6094	98.0	924	3	R10889	Leukotoxin 352 encode
15	6057	97.4	1098	21	W13866	Chimeric protein #1.
16	6050	97.3	1098	4	R22103	Bovine IL-2 - LKT fus
17	6047	97.3	1098	9	R52747	Bovine IL-2/LKT chime
18	6046	97.2	953	8	R43865	Leukotoxin protein.

19	6037	97.1	953	2	R07167	105kd PTX protein of
20	6037	97.1	953	11	R60072	PtxA protein of Paste
21	6022	96.9	953	3	R15159	Leukotoxin from P. ha
22	4925	79.2	934	20	W07637	P. suis leukotoxin ge
23	4254	68.4	956	25	W22156	ApxiIC protein.
24	4254	68.4	956	3	R12561	APPA haemolysin anti
25	2566	41.3	1049	25	W22159	ApxiIIB protein.
26	2566	41.3	1244	10	R54781	Leukotoxin AppliA.
27	2291	36.9	1022	25	W22152	ApxiA protein.
28	2244	35.1	1023	15	R76991	LhaA (low homology to
29	2223	35.8	544	19	W03943	LKT-GnRH protein fusi
30	2167	34.9	1334	10	R50290	lktA::lacZ fusion pro
31	2160	34.7	1334	3	R14481	lktA::lacZ fusion prod
32	2056	33.1	1403	3	R10890	lktA::lacZ fusion pro
33	1758	28.3	758	17	R85998	Enterohaemorrhagic E.
34	893	14.4	1522	2	P93357	Sequence of the catal
35	896	14.4	1705	2	P94365	Sequence of part of a
36	893	14.4	1706	2	R08031	Adenyl cyclase from B
37	885	14.2	1445	2	R12108	N-terminal deleted ad
38	433	7.3	1263	25	W13503	B. pertussis adenylcy
39	448	7.2	1262	25	W13505	B. bronchiseptica ade
40	440	7.1	1644	25	W13504	B. bronchiseptica ade
41	443	7.1	1645	25	W13502	B. pertussis adenylcy
42	281	4.5	127	15	R76990	Actinobacillus antige
43	276	4.4	900	4	R20568	Sequence of a partial
44	223	3.6	997	10	R54630	Mannuronan C-5-epimer
45	215	3.5	617	24	W27247	Pseudomonas fluoresce

ALIGNMENTS

RESULT 1  
 ID W03942 standard; Protein; 977 AA.  
 AC W03942;  
 DT 20-NOV-1996 (first entry)  
 DE LKT-GnRH protein fusion from pCB113.  
 KW Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;  
 KW fusion protein; immunogen; vaccine; fertility control;  
 KW contraceptive; sterilisation.  
 OS Chimeric Pasteurella haemolytica A1 strain B122;  
 OS Chimeric synthetic.  
 EH Key Location/Qualifiers  
 FT domain 1..929  
 FT /label= LKT  
 FT domain 927..977  
 FT /label= GnRH\_repeat\_domain  
 FT W09624675-A1.  
 PD 15-AUG-1996  
 PF 24-JAN-1996; CA0049.  
 PR 10-FEB-1995; US-387156.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Manns JG, Potter AA;  
 DR WPI: 96-384447/38.  
 DR N-PSDB: T37176.  
 PT Gonadotropin-releasing hormone multimer fusion proteins - with  
 PT leukotoxin polypeptide for increased immunogenicity, useful in  
 PT antifertility vaccine prodn.  
 PS Claim 7; Fig 5A-5H; 87pp; English.  
 CC A chimeric protein (W03942) is composed of a fusion between  
 CC also W03945) and a 4-copy gonadoliberin-releasing hormone (GnRH)  
 CC repeat sequence (see also W03944). It is the product of a  
 CC chimeric gene (T37176) produced by ligating a synthetic sequence  
 CC for the 4-copy GnRH into vector pAA352 (ATCC 68283), which carries  
 CC the LKT-352 gene. Recombinant plasmid pCB113 (LKT 352.4 copy  
 CC GnRH, ATCC 69749) was obt'd. Escherichia coli transformants  
 CC produced the chimeric protein, which is useful as a vaccine for  
 CC fertility control, esp. immunological sterilisation of  
 CC domestic or farm animals.  
 SQ Sequence 977 AA;

Query Match 100.0%; Score 6217; DB 19; Length 977;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches	936;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Db	1	matvldsfkgtgakkillyipqnydydteqngldlvkaaeelgievqreernniata	60						
Qy	1	MATVLDLSPFKTGAKKILYIPQNYDYDEQNGLDLVKAAEELGIEVQREERNNIATA	60						
Db	61	qtslgtlqtaigttergivilsapqdkllqktkagaglaesivqnankaktvlsqigs	120						
Qy	61	QTSLGTIQTAIQTERGIVLSAPQDKLLQKT KAGALGSAESIVQNANKAKTVLSGIQS	120						
Db	121	ilgsvlagmdldealnqnsqhalakagletnslentiansvktldfegqisqfsgkl	180						
Qy	121	ILGSVLAGMDLDEALQNNSQHAKAGLELTNSLIENTIANSVKTLDFEGEIQSFGSKL	180						
Db	181	qnkigtltgdklnkigldkagldvlgslgataalvldknastakvkgagfela	240						
Qy	181	QNIKGLTGLDKLNKIGLDKAGLDVLSGLSGATAALVLDKNASTAKKVGAGFELA	240						
Db	241	nvvgvgnitkavssyilaqrvaaaglsstgpaalvldknastakvkgagfela	300						
Qy	241	NOVVGVNITKAVSSYILAQRVAAGLSSTGPVAALVLDKNASTAKKVGAGFELA	300						
Db	301	esyaerfkklygdgdnllaeyqrgtgidasvtaintalaagvsaagsviaspia	360						
Qy	301	ESYAERFKKLYGDGDNLLAEYQRGTTIDASVTAINTALAAIAGVSAAGSVIASPIA	360						
Db	361	llvsgitgvtistilqyskqamfehvankhknkiveknhknkfyngdydarylanlqd	420						
Qy	361	LLVSGITGVISTILQYSKQAMFEHVAHNKIVEKNNHKNFYNGDYDARYLANLQD	420						
Db	421	nmkflnlnkelqaerviaitqqqwdmngldagisrlgekvlsqkayvdafeekghika	480						
Qy	421	NMKFLNLNKELQAEVIAITQQQWDDNNIGDLAGISRLGEKVLSQKAYVDAFECKHIKA	480						
Db	481	dklvldsangliidvsnsgkaktqhlfrtpltptgterrvqtgkyeytklknirvd	540						
Qy	481	DKLVLDLSANGLIIDVSNSGKAKTQHILFRTPLTPTGTERRVQTKYEYTKLKNIRVD	540						
Db	541	skwitdgaasftdltnvvqrgielidnagnvttkethkialklgegdndvfvsggttei	600						
Qy	541	SKWITDGAASFTDLTNVVQRIEIDNAGNVTKETRIIAKLGEGDNDVFGSGTTEI	600						
Db	601	dgegdyrvhysrgvgnaitdsketegsvtnrvfvetgkalhevtthaltvgnree	660						
Qy	601	DGEGDYRVHYSRGVGNAITDSETEGSGVTNRVETGKALHEVTTHALTGVNREE	660						
Db	661	kleyrhnnqhagyytkdtklaveiigtshndifksgkfndafnggvgvdtidngdn	720						
Qy	661	KIEYRHSNNQHAGYYTKDTLKAVEIIGTSHNDIFKSGKFNDAFNGGVDITDNGDN	720						
Db	721	drlfqgkgddildgngddfidgkgkndllhggkgddifvhrkgdndltdsdgndkls	780						
Qy	721	DRLFQGGKDDILDGNGDDFIDGGKGNLLHGGKGDIFVHRKGDNDITDSDGNDKLS	780						
Db	781	fsdsnlkldltfekvknlnvitskkekvtignvfreadfakvpykatkdekiesliqg	840						
Qy	781	FSDSNLKDLTFEKKVKNLNVTNSKKEKVTIGNVFRADFAKEVPYKATKDEKIEIIQ	840						
Db	841	ngeritskvddliakngkitqdeliskvvdnyellkshknvtnsldklissvsafssn	900						
Qy	841	NGERITSKVDDLIKNGKITQDELSKVVDNYELLKSHKNVTNSLDKLSSVSFTSSN	900						
Db	901	dsrnlvaptmsldqslslqfargshwsyglrpg	936						
Qy	901	DSRNLVAPTMSLDQSLSLQFARGSHWSYGLRPG	936						

RESULT 2

ID R34547 standard; Protein; 936 AA.  
AC R34547;  
DT 23-AUG-1993 (first entry)  
DE GnRH-leukotoxin gene fusion prod.  
KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;

gonadotropin releasing hormone; rotavirus viral protein 4;  
carrier protein; lactation; reproduction; SRIF.  
OS Synthetic.  
FH Key  
FT protein  
FT peptide  
FT peptide  
PN W09308290-A.  
PD 29-APR-1993.  
PF 15-OCT-1992; CA0449.  
PR 16-OCT-1991; US-779171.  
PR 14-OCT-1992; US-960932.  
PA (USA-) UNIV SASKATCHEWAN.  
PI Hughes HPA, Potter AA, Redmond MJ;  
DR WPI; 93-152482/18.  
DR N-PSDB; Q41322.  
PT Immunological carrier system with enhanced immunogenicity -  
PT comprises chimeric protein comprising leuco:toxin peptide or  
PT homologous protein fused to antigen esp. somatostatin or  
PT gonadotropin releasing hormone  
PS Example 2; Fig 8; 95pp; English.  
CC Oligonucleotides contg. sequences from bovine gonadotropin  
CC releasing hormone (GnRH) gene were constructed on a Pharmacia Gene  
CC Assembler using standard phosphoramidite chemistry. The oligo-  
CC nucleotides were annealed and ligated into vector pAA352 (contg.  
CC the Pateurella heamolytica leuco-toxin gene) which had been digested  
CC with BamHI. The ligated DNA was used to transform E. coli strain  
CC MH3000. Transformsants contg. the oligonucleotide inserts were  
CC identified by restriction endonuclease mapping and the recombinant  
CC plasmid designated pAA502. The chimeric protein produced from the  
CC plasmid works to bring about a larger immune response than the antigen  
CC alone, i.e. the leukotoxin works as a carrier protein.  
CC See also R34545-8.  
SQ Sequence 936 AA;

Query Match 99.6%; Score 6193; DB 7; Length 936;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 934; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db	1	matvldsfkgtgakkillyipqnydydteqngldlvkaaeelgievqreernniata	60
Qy	1	MATVLDLSPFKTGAKKILYIPQNYDYDEQNGLDLVKAAEELGIEVQREERNNIATA	60
Db	61	qtslgtlqtaigttergivilsapqdkllqktkagaglaesivqnankaktvlsqigs	120
Qy	61	QTSLGTIQTAIQTERGIVLSAPQDKLLQKT KAGALGSAESIVQNANKAKTVLSGIQS	120
Db	121	ilgsvlagmdldealnqnsqhalakagletnslentiansvktldfegqisqfsgkl	180
Qy	121	ILGSVLAGMDLDEALQNNSQHAKAGLELTNSLIENTIANSVKTLDFEGEIQSFGSKL	180
Db	181	qnkigtltgdklnkigldkagldvlgslgataalvldknastakvkgagfela	240
Qy	181	QNIKGLTGLDKLNKIGLDKAGLDVLSGLSGATAALVLDKNASTAKKVGAGFELA	240
Db	241	nvvgvgnitkavssyilaqrvaaaglsstgpaalvldknastakvkgagfela	300
Qy	241	NOVVGVNITKAVSSYILAQRVAAGLSSTGPVAALVLDKNASTAKKVGAGFELA	300
Db	301	esyaerfkklygdgdnllaeyqrgtgidasvtaintalaagvsaagsviaspia	360
Qy	301	ESYAERFKKLYGDGDNLLAEYQRGTTIDASVTAINTALAAIAGVSAAGSVIASPIA	360
Db	361	llvsgitgvtistilqyskqamfehvankhknkiveknhknkfyngdydarylanlqd	420
Qy	361	LLVSGITGVISTILQYSKQAMFEHVAHNKIVEKNNHKNFYNGDYDARYLANLQD	420
Db	421	nmkflnlnkelqaerviaitqqqwdmngldagisrlgekvlsqkayvdafeekghika	480
Qy	421	NMKFLNLNKELQAEVIAITQQQWDDNNIGDLAGISRLGEKVLSQKAYVDAFECKHIKA	480
Db	481	dklvldsangliidvsnsgkaktqhlfrtpltptgterrvqtgkyeytklknirvd	540



QY	481	DKLUVQJDSANGIIDSNSGKATQHILFPTPLTPTGTEHRRVQTKYEYITKLNIRVD	540
Db	541	swkItDgaassfIdltnvvgriGielDnagnvktKetkiaklgEdgdnnvfgsgtteei	600
QY	541	SWKITDGAASSFDLTNVVQRIEGLDNDAGNVTKEKIIAKLGEgDDNVFGSGTTEI	600
Db	601	dGeggydrVhysrgnYgalIdatKetegsgytvnrfvetgkhalhevsthtalvgnee	660
QY	601	DGEGGYDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGKALHEVSTHTALVGNREE	660
Db	661	kIeyrhshnqghagyyktDtlkaveeiIgtshndIfksgkfndaFnggDgvdtIdgndgn	720
QY	661	KIEYRSHNQHAGYYTKOTLKAVEEIIGTSHNDIFKSGKFNDAFNGGSGVDTIDGNDGN	720
Db	721	drIfegqGadIdlgngDgOfIdggkGndllhgkgddIfvhrKgdgndIdtDsdgndkls	780
QY	721	DRUFEGKGDDIIDLGGNGDDFIDGGKNDLLHGKGDDIFVHRKGDDNDIITDSDGNDKLS	780
Db	781	fdsdnlkIdItfekvkhnlvItnsKkekvItqIqwfreadfakEvPnyKatckDeIeeIqg	840
QY	781	FSDSNLKDLITFEKVKHNLVITNSKKEKVIQWFRREADFAKEVPNYKATCKDEIEEQ	840
Db	841	nGerItsgvddIdIakngnKitqdeIlskvDnyellkhsknvtnsldklIssvsaftasn	900
QY	841	NGERITSGVDDLIAGNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISVSAFTSSN	900
Db	901	dsrnlvIaptsmldqslslqfargsgqhsyglrpg	936
QY	901	DSRNLVAPTSMLDQSLSLQFARGSGQHSYGLRPG	936

### RESULT 3

RESULT 3  
ID R52748 standard; Protein: 1069 AA;

AC	R52748:	
AD	01-JUL-1994	(first entry)
DE	Bovine IFNgamma/LKT chimeric protein encoded by plasmid pAA497.	
DT	Bovine; interleukin-2; IL2; P. haemolytica; leukotoxin; LTK; IFN;	
KW	LtkA; chromosome walking; fusion protein; vaccine; interferon; gamma;	
KW	monoclonal; polyclonal; antibody.	
OS	Pasteurella haemolytica - chimera	
OS	Bos taurus - chimera.	
Key	Location/Qualifiers	
FT	peptide	1..926

FT	peptide	1.520	/note= "Recombinant leukotoxin peptide [split]"
FT	peptide	927..1069	

FT /note= "Bo

PN US5273889-A.

PD 28-DEC-1993.

PF 22-AUG-1990;

PR 22-AUG-1990; US-57130

PR 16-OCT-1991; US-777715.

PA (CIBA ) CIBA GEIGY CANADA

PA (UYSA-) UNIV SASKATCHEWAN.

PI Campos M, Hughes HPA, Potter

DR WPI; 94-006687/01.

DR N-PSDB; Q54213.

Immunogenic fusion p

leukotoxin - used in vaccines and to raise monoclonal and polyclonal antibodies

PT antibodies  
 Disclosure: Fig 7, 5600, Esalich

**Discipline**

CC This sequence represents a fusion  
CC (IFNgamma) and pasteurized bovine

CC (IFN $\gamma$ ) and Pasteurella haemolytica leukotoxin (LTk). The leukotoxin gene ltkA was isolated from a gene library of P

CC leukotoxin gene, *lckA*, was isolated from a gene library of *P. haemolytica* by chromosome walking. Immunogenic fusion proteins

haemolytica by chromosome walking. Immunogenic fusion proteins such as this can be used in vaccine compositions. It can also

CC such as this can be used in vaccine compositions. It can also  
CC used to raise mono- and polyclonal antibodies

50 . Sequence 1069 AA:  
access to large mono and polyclonal antibodies.

[illegible]

Query Match

Query Match	98.7%	Score 6135	DB 9	Length 1069
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches	927	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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Db	1	matvldlsfpkgtgakkililypnqnydydteqnglqdlvkaaeelgievqreernniata	60
Qy	1	MATVLDLSFPKTKAKKIIILYPONQYDTEQNGLDLVKAAEELGIEVQREERNNIATA	60
Db	61	qtslgtiqtaigitergivlsapdklllqktkagalsaesivqnankatvlsigis	120
Qy	61	QTSLGTIQTAIGITERGIVLSAPOIDKLQKTAGALSAESIVQNANKATVLSIGIOS	120
Db	121	ilgsvlagmdldealgnnsnqhalakagieltnslieniansvktldefgeqlsqfgskl	180
Qy	121	ILGSVLAGMDLDEALGNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKL	180
Db	181	qnkglgtlqdklkniggldkaglgldvsgllsgataalvladknastakvvgafjela	240
Qy	181	QNIKGLGTLDKLNIGGLDKAGLGLDVTSGLLSGATAALVLADKNASTAKVVGAFJELA	240
Db	241	nvvgvgnitkavssvllaqrvaaqlsgtgpvaalaaistvslaisplafagiackfnhaks	300
Qy	241	NOVVGVNITKAVSSVLLAQRVAAGLSGTGPVAALIAASTVSLAISPLAFAGIACKFNHAKSL	300
Db	301	esyaerfkllygdqdnllaeyrgtgtidasvtcainatalaaaggvysaaaagsvlaspia	360
Qy	301	ESYAERFKLGYDQDNLLAEYRGTGCTIDASVTAINTALAAAGGVYSAAAAGSVIASPIA	360
Db	361	llvsgitgvistilqyskqamfehvanklhnkiveweknnhknfyfengydarylanlqd	420
Qy	361	LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEKNNHKNFYFENGYDARYLANLOQ	420
Db	421	nmkflnlmlkelqaerviaitcqqvqdnngldlagisrlgekvlsghkayvdafeegkhika	480
Qy	421	NMKFLNLMLKELQAERVIAITQQQVQDNNGLDLAGISRLGEKVLSGHKAYVDAFEEGKHIIKA	480
Db	481	dklvqidsangiaadvnsngkaktqhilfrtpltptgterhrvqtgkyeyitklnlnrvd	540
Qy	481	DKLVQIDSANGIADVNSNGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYITKLNLRVD	540
Db	541	swkitdgaasstfdltnvvqrigieldnagnvttkktetkilaikleggdnnvfvgsgttei	600
Qy	541	SWKITDGAASSTFDLTNVVQRIGIELDNGAVTTKTKETKIIAKLGSGDNNVFVSGTTEI	600
Db	601	dgeegdyrvhysrgnygaltidatketegsvtyrnrfvetgkalhevtsthalvgnree	660
Qy	601	DGEGGIDRVHYSRGNYGALTI DATKETEGSVTYNRNFVETGKALHEVTSTHTALVGNREE	660
Db	661	kieyrhsmnqhaggyktdtklaveeligstshndifksgkfndafnggdvtdidngdn	720
Qy	661	KIEYRHSNNQHAGGYKTDPLKAVEEIICTSHNDIFKSGKFNDAFNGGDVTDIDNGDN	720
Db	721	drlfpgkgddildggngddfidggkndllhggkgddifvhrkgdndlitdsdgnkdis	780
Qy	721	DRLFGKGDDILDGGNGDDPIDGGKNDLLHGGKGDDIFVHRKGDCNDIITDSDGNDKDIS	780
Db	781	fsdsnlkdlitfekvkhnlvitnskketvliqvwfreadfakexpnykatkdekieleiigq	840
Qy	781	FSDSNLKDLITFEKVKNLNVITNSKKKEKVTIQNWFREADFAKEVPNYKATKDEKIEEIIIGQ	840
Db	841	ngeritskqvddliakngkitgdelskvvdyneyllikhknvnsidkklissvysatfssn	900
Qy	841	NGERITSKQVDDLIAGNGKITODELSKVVDYNEYLLKHKNVTNSLDKLISSVYSATFSSN	900
Db	901	dsrnvlvaptsmldqslslsqfargsq	927
Qy	901	DSRNLVAPTSMLDQSLSLSQFARGSQ	927

## RESULT

ID W13867 standard: Protein: 1069 AA.

W13867;  
AC

DT 12-MAY-1997 (first entry)

Chimeric protein #2.

KW RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; cytokine; vaccine; vaccine

KW interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumoñia;

KW Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;

22

KW fibrinous pneumonia; cattle; therapy.  
 OS Synthetic.  
 PN US5594107-A.  
 PD 14-JAN-1997. 571301.  
 PR 22-AUG-1990; US-571301.  
 PR 16-OCT-1991; US-777715.  
 PR 20-DEC-1993; US-170126.  
 PA (CIBA ) CIBA GEIGY CANADA LTD.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Campos M, Hughes HPA, Potter A;  
 DR WPI: 97-099529/09.  
 DR N-PSDB: T60033.  
 PT Immunogenic chimeric proteins comprising cytokine linked to RTX  
 toxin - useful in vaccines, esp. against shipping fever in cattle  
 PS Claim 13; Column 37-46; 56pp; English.  
 CC W13866 and W13867 represent immunogenic chimeric proteins of the  
 CC invention. This sequence represents a chimeric protein containing the  
 CC bovine gamma interferon (gamma IFN) sequence and a leukotoxin sequence.  
 CC The chimeric proteins of the invention comprise a cytokine, selected from  
 CC interleukin-2 (IL-2) and gamma IFN, linked to at least one RTX toxin  
 CC epitope (preferably the sequence shown in W13865). The RTX toxin used to  
 CC provide the epitope sequence is preferably a leukotoxin, especially the  
 CC full-length Pasteurella haemolytica leukotoxin. Alternatively, the  
 CC leukotoxin is a truncated leukotoxin lacking leukotoxic activity,  
 CC especially LKT352. The chimeric proteins can be used for the production  
 CC of vaccines against respiratory diseases such as pneumonia, particularly  
 CC fibrinous pneumonia caused by P.haemolytica, including shipping fever in  
 CC cattle.  
 SQ Sequence 1069 AA;

Query Match 98.7%; Score 6135; DB 21; Length 1069;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfpgtkakkililypqnyqydeqngldlvkaaeelgievqreernniata 60  
 |||||||  
 QY 1 MATVIDLSFPKTKAKKILILYIPQNYQYDEQNGLDLVKAAEELGIEVQREERNIATA 60  
 |||||||

Db 61 qtslgtiqtaigtergvlspapdkllqktkagaglsaesivqnankaktvlsqigs 120  
 |||||||  
 QY 61 QTSLGTIOAIGLTERGIVLSAPQIDKLQKTQKAGALSAESIVONANKAKTVLSGIQS 120  
 |||||||

Db 121 ilqsvlagmdlealonnshalakagieltnslieniansvktldfegdisfgskl 180  
 |||||||  
 QY 121 ILQSVLAGMDLEALONNSHALAKAGIELTNSLIENIANSVKTLDFEGDISFGSKL 180  
 |||||||

Db 181 qnikgigtldklniggidkaglgldvsgllsgataalviadknastakkvagafela 240  
 |||||||  
 QY 181 QNIKGIGTLGDLKNIKGGLDKAGLDLVISGLSGATAALVADKNASTAKKVAGAFELA 240  
 |||||||

Db 241 nqvvgnitkavssyllaqraaglstgtpvaalastvslaisplafagiadkfahksl 300  
 |||||||  
 QY 241 NQVVGNITKAVSSYILAQRAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFHAKSL 300  
 |||||||

Db 301 esyaerfkllygdgnllaeayrgtgtdasvtaintalaaaggvsaaasviaspia 360  
 |||||||  
 QY 301 ESYAERFKLGYDGNLLAEAYRGGTGTDASVTAIN TALAAAGGVSAAASVIASPIA 360  
 |||||||

Db 361 livsgitgvtistilqyskqamfehvankihnkliwvknhghknfyfengydarylanlqd 420  
 |||||||  
 QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKLIWVKNHGHKNFYFENGYDARYLANLQD 420  
 |||||||

Db 421 nmkflnlnkelgaerviaitgqqdnnlsgdlaglsrgekvlskayvdafeegkhika 480  
 |||||||  
 QY 421 NMKFLNLNKELGAERVIAITQQQDNNLSDLAGLSRGEKVL SKAYVDAFEEGKHKA 480  
 |||||||

Db 481 dklvqldsangiidvsnkaktqhilftpltpgttehrervqtkyeyiklinirvd 540  
 |||||||  
 QY 481 DKLVDQSANGIIDVSNKAKTQHILFTPLTPGTTEHREVRVQTKYEYIKLINIRVD 540  
 |||||||

Db 541 swkitdgaasstfdlnvvqrglgieidnagnvktktetkiaaklgdgdndvfvsggttei 600  
 |||||||

QY 541 SWKITDGAASSTFDLTVNVQRIGIELDNAGNVTKTKETIIAKLGGDDNVFVSGGTTEI 600  
 Db 601 dggegydrvrhysrgnygaltidatketegsytvnrnfvetgkalhevtstthalvgnree 660  
 |||||||  
 QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
 |||||||

Db 661 kievrhsonqhagyytkdtlkaveeiiigtshndifkqskfndafnggdvdtldgndgn 720  
 |||||||  
 QY 661 KIEVRHSONQHAGYYTKDTLKAVEEIIIGTSHNDIFKQSKFNDAFNGGDVDTLDGNDGN 720  
 |||||||

Db 721 drlfggkaddildgngdgdffidgkgndllhggkgddifvhrkgdndiildsgndkls 780  
 |||||||  
 QY 721 DRLFGKGDDIILDGNGDGFIDGKGNDLLHGGKGDDIFVHRKGDDIITDSDGNKLS 780  
 |||||||

Db 781 fdsnlkltfkvkhnlvitnskkvktlgnwfredafakevpykatkdeleelgq 840  
 |||||||  
 QY 781 FDSNLKLTPEKVKHNDVITNSKKVKTIQWFRADFAKEVPNYKATKDEKEIEIIGQ 840  
 |||||||

Db 841 ngeritsqvdllakngkitqdelkskvndynellkshkntvtsldklsvsafssn 900  
 |||||||  
 QY 841 NGERITSQVDDLLAKNGKITQDELSKVVDNYELLKSHKNTVTSLDKLSVSAFTSSN 900  
 |||||||

Db 901 dsrnvlvaptmldgslslgfgarsq 927  
 |||||||  
 QY 901 DSRNVLVAPTSMLDQSLSLGFARSGQ 927  
 |||||||

RESULT 5  
 ID R14482 standard; Protein; 926 AA.  
 AC R14482;  
 DT 15-JAN-1992 (first entry)  
 DE LKT352.  
 KW Antigen; leukotoxin; vaccine; lktA.  
 OS Pasteurella haemolytica.  
 PN WO9115237-A.  
 PD 17-OCT-1991.  
 PR 17-OCT-1991; CA0170.  
 PR 05-APR-1990; US-504850.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Acres SD, Bariuk LA, Potter AA, Lawman MJP;  
 DR WPI: 91-324967/44.  
 PT Vaccines for Pasteurella haemolytica infection in cattle -  
 PT comprise sub-unit antigens from P haemolytica fibrillar protein,  
 PT plasmin receptor, 50 K outer membrane protein and leukotoxin.  
 PS Disclosure; Fig 5; 92pp; English.  
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates  
 CC to the same position on gels.  
 CC The LKT352 gene was prep'd. as follows: lktA, an MaeI fragment  
 CC contg. the gene was ligated into the SmaI site of pUC13 to form  
 CC pAAL79. From this, two constructs were made in the pTac-based  
 CC vector, pOH432:laci digested with SmaI. One, pAA342, consisted of  
 CC the 5' AluII fragment from lktA while the other, pAA345, contained  
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated  
 CC leukotoxin peptide at high levels while pAA345 expressed full  
 CC length leukotoxin at very low levels. The 3' end of the lktA gene  
 CC of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to  
 CC yield pAA352 contg. the LKT352 sequence. The protein expressed  
 CC from the vector can be used to prepare a subunit vaccine with  
 CC other P. haemolytica antigens, e.g. fibrillar protein, plasmin  
 CC receptor or 50K outer membrane protein. The vaccines can be used  
 CC to protect cattle from respiratory diseases such as pneumonia, esp.  
 CC shipping fever pneumonia.  
 CC See also R14481, 83,84 and 85.  
 SQ Sequence 926 AA;

Query Match 98.6%; Score 6128; DB 3; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfpgtkakkililypqnyqydeqngldlvkaaeelgievqreernniata 60  
 |||||||  
 QY 1 MATVIDLSFPKTKAKKILILYIPQNYQYDEQNGLDLVKAAEELGIEVQREERNIATA 60  
 |||||||



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QY 481 DKLVQDSANGIIVDSNSGKATQHLLFTPLLTGTEHRRVQKVEYITKLNINRVD 540.
Db 541 swkitdgaasftdltnvvqrvgldnagnvktktetkilaaklgdgdnnvfvgsgttei 600
QY 541 SNKITDGAASFTDLTNVVQRVGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGTTEI 600
Db 601 dggegydrvhysrgnygaltidatketegsytvnrftvgkalhevtsthalvgnree 660
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGKALHEVSTHALVGNREE 660
Db 661 kleyrhshnnqhagyytkdtikaveeiiqtsndifksgkfndafngdgvdtidgndgn 720
QY 661 KLEYRHSNNQHAGYYTKDTLKAVEEIIQTSNDIFKSGKFNDAFNGDGVDTIDGNDGN 720
Db 721 drlfggkgddiildgngddfidggkgndllhggkgddifvhrkgdndiitdsdgnkls 780
QY 721 DRLFGGKGDDIILDGNGDDFIDGGKGNLHGGKGDDIFVHRKGDNDIITDSGDNKLS 780
Db 781 fdsnlkdltfekvkhnlvitnskketvtiqnwrfreadfakvnpnykatkdekieleiigq 840
QY 781 FDSNLKDLTFEKVKHNLVITNSKKEKVTIQNWFREADFAKEVPNYKATKDEKIEEIIQ 840
Db 841 ngeritskvddliakngkitqdelkskvdyvnyellkshkntnsldkllissvsafstsn 900
QY 841 NGERITSKVDDLIAKNGKITQDELSKVVDNYELLKSHKNVTNSLDKLISSVSFTSSN 900
Db 901 dsrnvlvaptsmldqslslqfargs 926
QY 901 DSRNVLVAPTSMLDQSLSLQFARGS 926

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RESULT 7

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AC R50291 standard; Protein: 926 AA.
DE Recombinant leukotoxin from plasmid PAA352.
KW Vaccine; outer membrane protein; OMP; Haemophilus somnus;
KW iron regulated protein; leukotoxin; Pasteurella haemolytica;
KW LKt352.
OS Pasteurella haemolytica A1 (strain B122).
PN CA2097707-A.
PD 03-JAN-1994.
PE 29-JUN-1993; 099707.
PR 02-JUL-1992; US-908253.
PA (UYSA-) UNIV SASKATCHEWAN.
PI Harland RJ, Potter AA;
DR WPI: 94-092909/12.
DR N-PSDB: Q44760.
PT Haemophilus somnus outer membrane protein extract -
PT enriched with iron-regulated proteins, opt. contg.
PT leuco:toxin antigens, for use as vaccine
PS Claim 5; Fig 5; 78pp; English.
CC A vaccine comprising an outer membrane protein (OMP) extract of
CC Haemophilus somnus enriched with iron regulated proteins is new.
CC The vaccine pref. further comprises an immunogenic leukotoxin
CC homologous to LKt352. Example 1.2 describes the prodn. of
CC P. haemolytica recombinant leukotoxin from PAA352.
CC Two expression constructs were made. One, PAA342, contained the
CC 5'-AhaiI fragment of the ltkA gene, while the other, PAA345,
CC contained the entire ltkA gene. PAA342 expressed a truncated
CC leukotoxin peptide at high levels, while PAA345 expressed full
CC length leukotoxin at very low levels. Therefore, the 3' end
CC of the ltkA gene was ligated into PAA342, yielding plasmid PAA352.
CC LKt352 or new leukotoxin is 98% homologous to authentic
CC leukotoxin.
CC NB: the protein sequence in Fig 5 comprises 926 amino acids,
CC however this protein is described in the text as having
CC 931 amino acids.
SQ Sequence 926 AA;

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Query Match 98.6%; Score 6128; DB 10; Length 926;

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Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 matvidlsfptgakkliilypqnyqdydtegnqlqdlvkaaeelievqreernniata 60
QY 1 MATVIDLSFPTGAKKLIILYPQNYQDYDTEGNGQLQDLVKAABEELGIEVQREERNNIATA 60
Db 61 qtslgtiqtalgltergivilsapqldklktkagqalgsaesivqnankaktvlgstqs 120
QY 61 QTSLGTTQTALGLTERGIVLSAPQIDKLKTKAGQALGSAESIVQNANKAKTVLSGTQS 120
Db 121 ilgsvlaqmdldealqnnsqhalakagleltnslieniansvktldfegqisqfgekl 180
QY 121 ILGSVLAQMDLDEALQNNSQHAKAGLELTNSLIENIANSVKTLDFEGQISQFGEKSL 180
Db 181 qnikglgtlqdklnigldkagldglvisgllsgataalvlnadknastakvvgafela 240
QY 181 QNIKGLGTLDKLNIGGLDKAGLDLVISGLLSGATAALVLADKNASTAKVVGAFELA 240
Db 241 nvvgnitkavssyilaqrvaaglsstgppvaallastvslaisplafagiadkfhnksl 300
QY 241 NOVVGNIITKAVSSYILAQORVAAGLSSTGPPVAALIASTVSLAISPLAFAGIADKFHNKSL 300
Db 301 esyaerfklkgddnllaeqrgtgidastaintalaaiaagvsaagviapla 360
QY 301 ESYAERFKLKGDDNLLAEQRGTGITIDASTAINTALAAIAGVSAAGSVIAPLA 360
Db 361 llvgitgvisitlqyskqamfehvankhknkiveweknnhgnkfengydarylanlqd 420
QY 361 LLVGSITGVIITLQYSKQAMFEHVANKHNKIVWEKNNHGNKFENGYDARYLANLQD 420
Db 421 nmkfillnlkelqaerviaitcqqqwdnnmigdagsrlrgekvlsqkayvdafeegkhika 480
QY 421 NMKFIILLNKELOAERVIAITCQQQWDNNMIGDAGSLRGEKVLSEKAYVDAFEEGKHICA 480
Db 481 dklvqlsdanglidvsnsgkaktchilfrtlltpgttehrervatgkyeytklinrvd 540
QY 481 DKLVLSDANGLIDVSNSGKAKTCHILFRTPLLTPGTTEHRRVOTGKYEYITKLNINRVD 540
Db 541 swkitdgaasftdltnvvqrvgldnagnvktktetkilaaklgdgdnnvfvgsgttei 600
QY 541 SWKITDGAASFTDLTNVVQRVGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGTTEI 600
Db 601 dggegydrvhysrgnygaltidatketegsytvnrftvgkalhevtsthalvgnree 660
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGKALHEVSTHALVGNREE 660
Db 661 kleyrhshnnqhagyytkdtikaveeiiqtsndifksgkfndafngdgvdtidgndgn 720
QY 661 KLEYRHSNNQHAGYYTKDTLKAVEEIIQTSNDIFKSGKFNDAFNGDGVDTIDGNDGN 720
Db 721 drlfggkgddiildgngddfidggkgndllhggkgddifvhrkgdndiitdsdgnkls 780
QY 721 DRLFGGKGDDIILDGNGDDFIDGGKGNLHGGKGDDIFVHRKGDNDIITDSGDNKLS 780
Db 781 fdsnlkdltfekvkhnlvitnskketvtiqnwrfreadfakvnpnykatkdekieleiigq 840
QY 781 FDSNLKDLTFEKVKHNLVITNSKKEKVTIQNWFREADFAKEVPNYKATKDEKIEEIIQ 840
Db 841 ngeritskvddliakngkitqdelkskvdyvnyellkshkntnsldkllissvsafstsn 900
QY 841 NGERITSKVDDLIAKNGKITQDELSKVVDNYELLKSHKNVTNSLDKLISSVSFTSSN 900
Db 901 dsrnvlvaptsmldqslslqfargs 926
QY 901 DSRNVLVAPTSMLDQSLSLQFARGS 926

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RESULT 8

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ID R42378 standard; Protein: 924 AA.
AC R42378;
DT 19-APR-1994 (first entry)
DE Recombinant leukotoxin peptide (split) from plasmid pGCH5.

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KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;  
 KW thromboembolic meningococcalitis; septicaemia; arthritis;  
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.  
 OS Pasteurella haemolytica.  
 PN W09321323-A.  
 PD 28-OCT-1993.  
 PF 05-APR-1993; CA0135.  
 PR 09-APR-1992; US-865050.  
 PR 04-JUN-1992; US-893424.  
 PR 04-JUN-1992; US-893426.  
 PR 29-MAR-1993; US-038287.  
 PR 29-MAR-1993; US-038288.  
 PR 29-MAR-1993; US-038719.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;  
 PI Rioux C, Theisen M;  
 DR N-PSDB; Q51081.  
 PT Haemophilus somnus immunogenic proteins used in vaccines -  
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,  
 PT and corresp. DNA  
 PS Disclosure; Fig 5; 119pp; English.  
 CC The hmb gene encoding the haemin-binding protein was expressed in  
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene  
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken  
 CC from PRAP501 and starts at the codon for the third amino acid residue  
 CC of ORF1. The haemin binding protein can be used in vaccines for  
 CC preventing or treating H. somnus infections, which cause thromboembolic  
 CC meningococcalitis, septicaemia, arthritis and pneumonia in  
 CC vertebrates.  
 CC See also R42370-86.  
 SQ Sequence 924 AA;  
 Query Match 98.4%; Score 6117; DB 8; Length 924;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 matvidsfpktaakliipqnyqydeqngldlvkaaeelgievqreenniaata 60  
 QY 1 MATVIDLSFPKTKAKKILIPQNYQYDEQNGLDLVKAAEELGIEVQREENNIAATA 60  
 Db 61 qtslgtiqtaigtergivasqdkilgktkagalgasaeivqpankaktvslgigs 120  
 QY 61 QTSLGITQTAIGTERGIVLSAQIDKLLQKTAKGALGSAESIVQNAKAKTVLSGIQS 120  
 Db 121 ilgsvlagmdldealqnsnqhalakagleitnslieniansvktldefgeqisqfsgkl 180  
 QY 121 ILGSLAGMDLDEALQNSNOHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFSGKL 180  
 Db 181 qnikgltigdklknigldkaglgldvisgllsgataalvladknaastakkvagfela 240  
 QY 181 QNIKGTLGLDKLNTGGDLKAGLDLVISGLSGATAALVLADKNASTAKKVAGGFELA 240  
 Db 241 nqvvgnitkavssvilaqrvaaglstgqpvaaiaiascvslaisplafagiadkfnhaks1 300  
 QY 241 NOVVGNTKAVSSVILAQRVAAGLSSTGQPVAAIAISTVLSAISPLAFAGIADKFNHAKSL 300  
 Db 301 esyaerfkilgydgnllaeyqrgrgtgtidasvtaintalaaiaaggvsaaagsviaspia 360  
 QY 301 ESYAERFKILGYDGNLLAEYQRGTGTIDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360  
 Db 361 llvsgitgvtistilqysqamfahvankhmkiveknhngknyfengydarylanlqd 420  
 QY 361 LLVSGITGVTISTILOYSQAMFAHVANKHMKIVEKNHNGKNYFENGYDARYLANLQD 420  
 Db 421 nmkfllnlmkelaerviaitqgqndnigdlagisrlgekvlskayvdafegkhika 480  
 QY 421 NMKFLNLNKLQARVIAITQQQNDNIGDLAGISRLGEKVLSKAYVDAFEGKHika 480  
 Db 481 dklvqidsangiidvsnsgkaktghilfrptlltpgttehrvrtgkyeyitklninrvd 540  
 QY 481 DKLVLQDSANGIIDVSNSGKAKTGHILFRPTLLTPGTEHREVRTGKYEYITKLNINRVD 540

Db 541 swkitdgaasstfdlnnvqrigieldnagnvntkktetkialkagddnfvsgsttei 600  
 QY 541 SWKITDGAASSTFDLNNVQRIEILDNAGNVTKTETKIIAKLGGDDNVFVSGSTTEI 600  
 Db 601 dggegydrvhysrgnygaltidatketegsytvnrftvetgkalhevtsthtalvgnree 660  
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETECSYTVNRFVETGKALHEVSTHTALVGNREE 660  
 Db 661 kleyrhnsnqhagyytkdtklaveeiigtshndifksgkfndafnggvgvtdidndgn 720  
 QY 661 KIEYRHNSNQHHAGYYTKDTKLAVEEIICTSHNDIFKSGKFNDAFNGGVGVDIDNDGN 720  
 Db 721 drlfkgkgddilidgngddfidgkgndilhqgkaddifvhrkgdndiitdsdgnkls 780  
 QY 721 DRLFGKGDDIILIDGNGDDFIDGKGNDILHQGKDDIFVHRKGNDIITDSDGNDKLS 780  
 Db 781 fadsnlkdlitfekvkhnlvitnskketvignwfreadfavepnykatkdekiesliqg 840  
 QY 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWREADFAKEVPNYKATKDEKIEIIGQ 840  
 Db 841 ngeritskvddliakngkitqdelkskvvdyellkhsknvtnsldklissvsafstsn 900  
 QY 841 NGERITSKVDDLIKNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISVSFAFTSSN 900  
 Db 901 dsrnvlvaptmsldqslslqfar 924  
 QY 901 DSRNVLVAPTMSLDQSLSLQFAR 924  
 RESULT 9  
 ID R42380 standard; Protein; 924 AA.  
 AC R42380;  
 DT 19-APR-1994 (first entry)  
 DE Recombinant leukotoxin peptide (split) from plasmid pGCH4.  
 KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;  
 KW thromboembolic meningococcalitis; septicaemia; arthritis;  
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.  
 OS Pasteurella haemolytica.  
 PN W09321323-A.  
 PD 28-OCT-1993.  
 PF 05-APR-1993; CA0135.  
 PR 09-APR-1992; US-865050.  
 PR 04-JUN-1992; US-893424.  
 PR 04-JUN-1992; US-893426.  
 PR 29-MAR-1993; US-038287.  
 PR 29-MAR-1993; US-038288.  
 PR 29-MAR-1993; US-038719.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;  
 PI Rioux C, Theisen M;  
 DR N-PSDB; Q51082.  
 PT Haemophilus somnus immunogenic proteins used in vaccines -  
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,  
 PT and corresp. DNA  
 PS Disclosure; Fig 6; 119pp; English.  
 CC The hmb gene encoding the haemin-binding protein was expressed in  
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene  
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken  
 CC from PRAP504 and starts at the codon for the 33 rd amino acid residue  
 CC of ORF1. The haemin binding protein can be used in vaccines for  
 CC preventing or treating H. somnus infections, which cause thromboembolic  
 CC meningococcalitis, septicaemia, arthritis and pneumonia in  
 CC vertebrates.  
 CC See also R42370-86.  
 SQ Sequence 924 AA;  
 Query Match 98.4%; Score 6117; DB 8; Length 924;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 matvidsfpktaakliipqnyqydeqngldlvkaaeelgievqreenniaata 60  
 QY 1 MATVIDLSFPKTKAKKILIPQNYQYDEQNGLDLVKAAEELGIEVQREENNIAATA 60

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QY 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGQLDLVKAABEELGIEVQREERNNIATA 60
Db 61 qtslgtigtaltgtergvlslapqldkllqktkagaalgaesivqnankaktvlsqigs 120
QY 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGALGAESIVQNANKAKTVLSGIQS 120
Db 121 ilgsvlagmdldeallqnnsqhalakagletnslentieniansvktldfegqisqfsgkl 180
QY 121 ILGSLVAGMDLDEALQNNSQHAKAGAGLETNSLIENIANSVKTLDfEGQISQFGSKL 180
Db 181 qniklgltgdklknigglidagldvsgatlaalvldadnastakvgaagfela 240
QY 181 QNIKLGTLGDKLKNIGGLDLAGLDVSLGSLGATAALVLDADNASTAKVGAAGFELA 240
Db 241 ngvvgnitkavssylagrvaaaglstgtpvaalvastvslaisplafagiadkfnhaks 300
QY 241 NGVVGNTKAVSSYILAQRVAAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 esyaerfkklydgdnlleaygrgtidastvaintalaaiaaggvsaaagsviaspia 360
QY 301 ESYAERFKKLYDGDNLLEAYGRGTIDASTVAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 llvsgitgvtistilqyskqamfehvankihnkiveweknnhgknyfengydarylanlqd 420
QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYLANLQD 420
Db 421 nmkflnlmkelqaerviaitqggwdnnigdlaglsrlgekvlsqkayvdafeegkhika 480
QY 421 NMKFLNLNKELOAERVIAITQQQWNNIGDLAGLSRLGEKVLSQKAYVDAFEEGKHika 480
Db 481 dklvqldsangliidvsnsgkaktqhilfrtllptgterervqtgkyeytklinrvd 540
QY 481 DKLVQLDSANGLIIDVNSGKAKTQHILFRTPLLTPGTERERVQTGKYEYITKLINRVD 540
Db 541 swkitdgaasftldtnvvqrigieldnagnvktkettiaklgegdndvfvsgtteei 600
QY 541 SWKITDGAASFTLDTNVVRIGIELDNAGNVKTKETKIIAKLGEGDNDVFGSGTTEI 600
Db 601 dggegydrvhysrgnygaltidatketegsytnrvfvetgkalhevtsthtalvgnree 660
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTNRVFVETGKALHEVSTHTALVGNREE 660
Db 661 kleyrhnsnqhagyytktlkaveeiictshndifkgskfndafngdvgdtidngdn 720
QY 661 KLEYRHNSNQHAGYYTKTLKAVEEIICTSHNDIFKGSKFNDAFNGDVGDTIDNGDN 720
Db 721 drlfgkgddiildgngddfidgkgkndllhggkgddifvhrkgdndiitdsdgnkls 780
QY 721 DRLFGKGDDIILDGNGDDFIDGGKGNDDLHGGKGDDIFVHRKGDNDIITDSGDNKLS 780
Db 781 fdsnlkldltfekkhnvltnvtskkekvtiqnrfreadfakvppnykatkdekielelqg 840
QY 781 FSDSNLKDLTFEKKHNLVITNSKKEKVTIQNRFREADFAKVPVNYKATKDEKIEELIQQ 840
Db 841 ngeritskvoddliakngkiktdelskvdyellkhekntslndkllissvsftasn 900
QY 841 NGERITSKVODDLIAKNGKIKITDELSKVVDYELLKHSKNVTNSLDKLISSVSFTASN 900
Db 901 dgrnvlvaptmldgsslsqfar 924
QY 901 DSRNVLVAPTMLDQSSLSQFAR 924
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RESULT 10

ID R42385 standard; Protein; 924 AA.

AC R42385;

DT 19-APR-1994 (first entry)

DE Recombinant leukotoxin peptide from plasmid pCR28.

KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;

KW thromboembolic meningoenophthalitis; septicemia; arthritis;

OS pneumonia; lktA gene; haemin-binding protein; fusion protein.

PN Pasteurella haemolytica.

PN W09321323-A.

```
PD 28-OCT-1993.
PF 05-APR-1993; CA0135.
PR 09-APR-1992; US-865050.
PR 04-JUN-1992; US-893424.
PR 04-JUN-1992; US-893426.
PR 29-MAR-1993; US-038287.
PR 29-MAR-1993; US-038288.
PR 29-MAR-1993; US-038719.
PA (UYSA-) UNIV SASKATCHEWAN.
PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI Rioux C, Theisen M;
DR WPI: 93-351733/44.
DR N-PSDB; Q51086.
PT Haemophilus somnus immunogenic proteins used in vaccines -
PT selected from haemin-binding protein, haemolysin, LppB and LppC,
PT and corresp. DNA
PS Disclosure: Fig 11; 119pp; English.
CC The lppB gene protein was expressed in E. coli as a fusion to the
CC pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
CC pAA352. The lppB gene fragment was taken from pMS11. LppB can be
CC used in vaccines for preventing or treating H. somnus infections,
CC which cause thromboembolic meningo-encephalitis, septicemia, arthritis
CC and pneumonia in vertebrates.
CC See also R42370-86.
SQ Sequence 924 AA;
```

Query Match 98.4%; Score 6117; DB 8; Length 924;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 qtslgtigtaltgtergvlslapqldkllqktkagaalgaesivqnankaktvlsqigs 120
QY 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGALGAESIVQNANKAKTVLSGIQS 120
Db 121 ilgsvlagmdldeallqnnsqhalakagletnslentieniansvktldfegqisqfsgkl 180
QY 121 ILGSLVAGMDLDEALQNNSQHAKAGAGLETNSLIENIANSVKTLDfEGQISQFGSKL 180
Db 181 qniklgltgdklknigglidagldvsgatlaalvldadnastakvgaagfela 240
QY 181 QNIKLGTLGDKLKNIGGLDLAGLDVSLGSLGATAALVLDADNASTAKVGAAGFELA 240
Db 241 ngvvgnitkavssylagrvaaaglstgtpvaalvastvslaisplafagiadkfnhaks 300
QY 241 NGVVGNTKAVSSYILAQRVAAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 esyaerfkklydgdnlleaygrgtidastvaintalaaiaaggvsaaagsviaspia 360
QY 301 ESYAERFKKLYDGDNLLEAYGRGTIDASTVAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 llvsgitgvtistilqyskqamfehvankihnkiveweknnhgknyfengydarylanlqd 420
QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYLANLQD 420
Db 421 nmkflnlmkelqaerviaitqggwdnnigdlaglsrlgekvlsqkayvdafeegkhika 480
QY 421 NMKFLNLNKELOAERVIAITQQQWNNIGDLAGLSRLGEKVLSQKAYVDAFEEGKHika 480
Db 481 dklvqldsangliidvsnsgkaktqhilfrtllptgterervqtgkyeytklinrvd 540
QY 481 DKLVQLDSANGLIIDVNSGKAKTQHILFRTPLLTPGTERERVQTGKYEYITKLINRVD 540
Db 541 swkitdgaasftldtnvvqrigieldnagnvktkettiaklgegdndvfvsgtteei 600
QY 541 SWKITDGAASFTLDTNVVRIGIELDNAGNVKTKETKIIAKLGEGDNDVFGSGTTEI 600
Db 601 dggegydrvhysrgnygaltidatketegsytnrvfvetgkalhevtsthtalvgnree 660
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTNRVFVETGKALHEVSTHTALVGNREE 660
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Db 661 kievrsnqhagyytkdtlkaveeigtshndifksgkfnadafngdgvdtidngdn 720  
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 Db 721 drlfggkgddildegngddfidgkgkgnldllhggkgddifvhrkgdgnnditdsdgnkls 780  
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 Db 781 fsdenldlfevkhnvlvntskskkvtnqwfresdfakevnykatdekieleiig 840  
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 Db 841 ngeritskvddliakngkitdelkskvndyellkhsknvtnsldklissvsaftsn 900  
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 Db 901 dsrnlvaptsmldqslsslqfarg 924  
 QY 901 DSRNLVAPTSMLDQSLSSLQFARG 924

## RESULT 11

ID W03945 standard; Protein; 926 AA.  
 AC W03945;  
 DE 20-NOV-1996 (first entry)  
 DE P. haemolytica truncated leukotoxin (LKT352).  
 KW Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;  
 KW fusion protein; immunogen; vaccine; fertility control;  
 KW contraceptive; sterilisation; plasmid pAA352.  
 OS Pasteurella haemolytica A1 strain B122.  
 PN W0624675-A1.  
 PD 15-AUG-1996.  
 PF 24-JAN-1996; CA0049.  
 PR 10-FEB-1995; US-387156.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Manns JG, Potter AA;  
 DR WPI: 96-384447/38.  
 DR N-PSDB: T37179.  
 PT Gonadotropin-releasing hormone multimer fusion proteins - with  
 PT leukotoxin polypeptide for increased immunogenicity, useful in  
 PT antiferility vaccine prodn.  
 PS Example 1: Fig 3A-3I: 87pp: English.  
 CC A truncated leukotoxin (W03945), LKT 352, lacks the cytotoxic  
 CC portion of the native protein from Pasteurella haemolytica. It is  
 CC the product of plasmid pAA352 which carries a truncated lktA gene  
 CC (T37179). A fusion protein (W03942) between LKT352 and a  
 CC gonadotropin releasing hormone tetramer can be expressed in  
 CC Escherichia coli. This is useful as a vaccine for fertility  
 CC control, partic. immunological sterilisation of domestic or  
 CC farm animals.  
 SQ Sequence 926 AA;

Query Match 98.4%; Score 6119; DB 19; Length 926;  
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
 Matches 924; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfptgagkaiilypqnyqydtceggnglqlvkaaeelgievgreernniata 60  
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 Db 61 qtslgtiqatigtergivilsapidkllktkagqalgsaesivqpankaktvlsiqs 120  
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 Db 121 ilgsvlagmdldaalqnnqnqhalakagletnslslieniansvktldefgeqisqfkskl 180  
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 Db 181 qnikglgtlqdklknigldkaglgldvisgllsgataalvldknastakkvagfela 240  
 QY 181 QNIKGLGTLDKLNIGLDKAGLGLDVISGLLSGATAALVLDKNASTAKKVAGFELA 240

Db 241 nqvvgntkavssyilaqrvaaglsqtpvaaliastvslaisplafagiadkfnhaks 300  
 QY 241 NQVVGNTKAVSSYILAQ RVAAGLSQTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
 Db 301 esyaerfkklgydgnllaeayqrgrgtidasvtaintalaaiaaggvsaaaagsviaspia 360  
 QY 301 ESYAERFKKLGYDCDNLAEAYQRGTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360  
 Db 361 llvsgitgwtistilqyskamfehvanhkmkiveknnhknkfngydyarlanld 420  
 QY 361 LLVSGITGWTISTILQYSKAMFEHVANKHMKIVEKNNHKNKFNGYDYARLANLD 420  
 Db 421 nmkfllnlnlkeiaerviaitqgqwnnigdlagisrlgekvlsqkayvdafeegkhika 480  
 QY 421 NMKFLNLNKLKEIAERVIAITQQQWNNIGDLAGISRLGEKVLSSKAYVDAFEEGKHKA 480  
 Db 481 dklvqlidsangiidvsnsgkaktqhilfrtlltpgttehrervvtgkyeyitklnnrvd 540  
 QY 481 DKLVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRRVQTGKYEYITKLNINRVD 540  
 Db 541 swkitdgaasstfdltnvvqrigieldnagnvctketkiaklgegdndvfvsggttei 600  
 QY 541 SWKITDGAASSTFDLTNNVQRIEILDNAGNVCTKETKIIAKLGEGDNDNVFVSGGTTEI 600  
 Db 601 dggegdrvhyrsgnygaltidatketegsytvnr-fvetgtalhevtsthtalvgnee 660  
 QY 601 DGEGEDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGTALHEVTSTHTALVGNREE 660  
 Db 661 kievrsnqhagyytkdtlkaveeigtshndifksgkfnadafngdgvdtidngdn 720  
 QY 661 KIEVRSHNNQHAGYYTKDTLKAVEEIGTSHNDIFKSGKFNADAFNGDGVDTIDNGDN 720  
 Db 721 drlfggkgddildegngddfidgkgkgnldllhggkgddifvhrkgdgnnditdsdgnkls 780  
 QY 721 DRLFGGKGDDILDEGNGDDFIDGKGKGNLDLLHGGKGDDIFVHRKGDNNDITDSGDNKLS 780  
 Db 781 fsdenldlfevkhnvlvntskskkvtnqwfresdfakevnykatdekieleiig 840  
 QY 781 FSDSNLKDLEFEVKHNLVNTSKSKKVTNQWFRSDFAKEVNPYKATDEKIEEIIIG 840  
 Db 841 ngeritskvddliakngkitdelkskvndyellkhsknvtnsldklissvsaftsn 900  
 QY 841 NGERITSKVDDLIKNGKITDELKSKVNDYELLKHSKNVTNSLDKLISSVSAFTSN 900  
 Db 901 dsrnlvaptsmldqslsslqfarg 926  
 QY 901 DSRNLVAPTSMLDQSLSSLQFARG 926  
 RESULT 12  
 ID R34546 standard; Protein; 943 AA.  
 AC R34546;  
 DT 23-AUG-1993 (first entry)  
 DE Somatostatin-leukotoxin gene fusion prod.  
 KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;  
 KW gonadotropin releasing hormone; rotavirus viral protein 4;  
 KW carrier protein; lactation; reproduction; SRIF.  
 OS Synthetic.  
 FH Key  
 FT protein Location/Qualifiers  
 FT peptide /note= "recombinant leukotoxin protein"  
 FT 930..943  
 FT /note= "SRIF"  
 PN W09308290-A.  
 PD 29-APR-1993.  
 PF 15-OCT-1992; CA0449.  
 PR 16-OCT-1991; US-779171.  
 PR 14-OCT-1992; US-960932.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Hughes HPA, Potter AA, Redmond MJ;  
 DR WPI: 93-152482/18.  
 DR N-PSDB: Q41321.  
 PT Immunological carrier system with enhanced immunogenicity -







QY 901 DSRNVLVAPTSLDQSLSLQFARGS 926  
 |||

## RESULT 15

ID W13866 standard; Protein; 1098 AA.  
 AC W13866;  
 DT 12-MAY-1997 (first entry)  
 DE Chimeric protein #1.  
 KW RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;  
 KW interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;  
 KW Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;  
 KW fibrous pneumonia; cattle; therapy.  
 OS Synthetic.  
 PN US594107-A.  
 PD 14-JAN-1997.  
 PF 22-AUG-1990; 571301.  
 PR 22-AUG-1990; US-571301.  
 PR 16-OCT-1991; US-77715.  
 PR 20-DEC-1993; US-170126.  
 PA (CIBA ) CIBA GEIGY CANADA LTD.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 PI Campos M, Hughes HPA, Potter A;  
 DR WPI; 97-095529/09.  
 DR N-PSDB; T60032.  
 PT Immunogenic chimeric proteins comprising cytokine linked to RTX  
 PT toxin - useful in vaccines, esp. against shipping fever in cattle.  
 PS Claim 10; Column 25-32; 5pp; English.  
 CC W13866 and W13867 represent immunogenic chimeric proteins of the  
 CC invention. This sequence represents a chimeric protein containing the  
 CC bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The  
 CC chimeric proteins of the invention comprise a cytokine, selected from  
 CC IL-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin  
 CC epitope (preferably the sequence shown in W13865). The RTX toxin used to  
 CC provide the epitope sequence is preferably a leukotoxin, especially the  
 CC full-length Pasteurella haemolytica leukotoxin. Alternatively, the  
 CC leukotoxin is a truncated leukotoxin lacking leukotoxic activity,  
 CC especially LKT352. The chimeric proteins can be used for the production  
 CC of vaccines against respiratory diseases such as pneumonia, particularly  
 CC fibrinous pneumonia caused by P. haemolytica, including shipping fever in  
 CC cattle.  
 SQ Sequence 1098 AA;

Query Match 97.4%; Score 6057; DB 21; Length 1098;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 183 ktgakkilypqnyqdyteggnglqdvkaeeelgievqreernniatagtslgtqta 242  
 QY 11 KTGAKKILYIPQNYQDYTEGGNGLDLVKAAEELGIEVQREERNNIATAGTSLGTIOTA 70  
 Db 243 igltergivleapqdkllqktkagalgasiesivqnankaktvlsigslgsvlagmd 302  
 QY 71 IGLTERGIVLSAPQDKLLQKTKAGALGSABESIVONANKAKTVLSIGSLGVLGMD 130  
 Db 303 idealqnsnqhalakagleltnslieiansvktldfgeqisqfsgsklnikgltg 362  
 QY 131 LDEALQNSNQHALAKAGLELTNLSLIEANSVKYTLDFEGEIQSGKLQNIKRLGLTGL 190  
 Db 363 dklknigglkagldvlgslgataalvldknastakkvagfelangvgnitka 422  
 QY 191 DYKKNIGGLDRAGLDGVISGLLSGATLAALVLDKNASTAKKVAGFELANQVGNITKA 250  
 Db 423 vssyilagrvaaaglstgvpvaaliastvslaisplafagiadkfnhakslesyaerfkl 482  
 QY 251 VSSYILAQRVAAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLESYAEERFKL 310  
 Db 483 gydgnlllaevqrgtgtidasvtaintalaaagvsaaagsviaspiallvsgitgvi 542  
 QY 311 GYDGNLLAEXYORGTTIDASVTAINALAAAGVSAAAAGSVIASPIALLVSGITGVI 370  
 Db 543 stilgysqamfehvanhknkiveeknnhgnknyfengydarylanlqdmkflnlnk 602  
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Search completed: Wed Dec 9 19:19:58 1998  
 Job time : 242 secs.

QY 371 STILOYSQAMFEHVANKIHNKIVVEKNHGNKNYFENGYDARYLANLQDNMKFLLNKN 430  
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 QY 431 ELQAEVIAITQQQWDDNNIGDLAGISRLGEKVLGSKAYVDAFEKGKHAKADKLVLQDSAN 490  
 Db 663 giidvsnsgaktqhilfrtpellcpgtehrervqtgkyeyitklninorvswkltddaas 722  
 QY 491 GIIDVNSGKAKTOHILFRTPLLTPGTEHREVRVQTGKYEYITKLNINRVDSWKITDGAAS 550  
 Db 723 stfdltvqvrigtelndagnvktketkiaklqegddnvfvsggtteidggeggyrvh 782  
 QY 551 STFDLTNVVQRIGIELDNAGNVYTKETKIAKLGEGDDNVFVSGGTTEIDGGEgyrvh 610  
 Db 783 ysrgnygaltidatketeggsyvtvnrfvetgkhalhevtsthtalvgnreekieyrhannq 842  
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 Db 843 hhagyytkdtlkaveeeligtsghndifkgskfndafngggdvdtidgndgndrlfvgkgdd 902  
 QY 671 HHAGYTTKDTLKAYEEIIGTSHNDIFKGSKFNDAFNGGGDVDTIDGNDGNDRLFGKGDD 730  
 Db 903 ildegngddfidgkgkgnllhggkgddgifvhrkgdgnidiitdsdgncklsfsgsnlkdlt 962  
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 Db 1083 smldqslssllqfargs 1098  
 QY 911 SMLDQSLSSLLQFARGS 926

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:20:16 1998; MasPar time 33.89 Seconds  
Tabular output not generated. 942.937 Million cell updates/sec

Title: >US-08-455-970-12  
Description: (1-936) from US08455970.pep  
Perfect Score: 6217  
Sequence: 1 MATVIDLSFPKTKAKKIILY.....LSSLOFARGSQHWSYGLRPG 936

Scoring table: PAM 150  
Gap 11

Searched: 107076 seqs, 34141958 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir56  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 55.004; Variance 163.629; scale 0.336

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6037	97.1	953	1	B30169 leukotoxin A - Pasteu	0.00e+00
2	5510	88.6	955	1	A35254 leukotoxin A - Pasteu	0.00e+00
3	4254	68.4	956	1	B33389 toxin II - Actinobaci	0.00e+00
4	4198	67.5	956	1	A43834 toxin II - Actinobaci	0.00e+00
5	2616	42.1	1052	1	B49219 toxin III - Actinobac	0.00e+00
6	2566	41.3	1049	1	S51784 toxin III - Actinobac	0.00e+00
7	2398	38.6	1023	1	LECA hemolysin A - Escheri	0.00e+00
8	2385	38.4	1024	2	S10056 hemolysin A - Escheri	0.00e+00
9	2321	37.3	998	2	I41078 hemolysin - Escherich	4.17e-299
10	2291	36.9	1022	1	I39643 RTX-toxin I - Actinob	7.96e-295
11	2207	35.5	1055	1	A37205 leukotoxin A - Actino	7.59e-283
12	1208	19.4	208	2	S34238 leukotoxin A - Pasteu	1.43e-141
13	896	14.4	1705	1	OFBRC cyclolysin - Bordetel	2.76e-98
14	887	14.3	1706	2	S51672 adenylate cyclase hem	4.77e-97
15	286	4.6	1829	2	S35027 cytotoxin RTX homolg	7.59e-18
16	265	4.3	1115	2	A47058 Fe-regulated RTX cyto	2.37e-15
17	221	3.6	835	2	J66140 cell surface-associat	2.75e-10
18	224	3.6	991	2	I39739 mannuronan C5 epimer	1.27e-10
19	217	3.5	597	2	S74999 iron-regulated protei	7.71e-10
20	203	3.3	1741	2	S74910 hemolysin - Synecchoc	2.71e-08
21	187	3.0	476	2	A43942 lipase - Pseudomonas	1.44e-06
22	173	2.8	284	2	S98385 nodo protein - Rhizob	4.21e-05
23	173	2.8	284	2	A43721 nodule formation prot	4.21e-05

24	165	2.7	475	2	S48132 metalloproteinase G (	2.76e-04
25	166	2.7	479	2	A38307 metalloproteinase C (	2.19e-04
26	170	2.7	481	2	A33712 metalloproteinase B (	8.55e-05
27	169	2.7	1771	2	S76851 hypothetical protein	1.08e-04
28	164	2.6	472	2	A30160 metalloproteinase (EC	3.48e-04
29	162	2.6	478	2	A36137 metalloproteinase (EC	5.53e-04
30	160	2.6	613	2	J50763 triacylglycerol lipas	8.77e-04
31	164	2.6	1290	2	S76853 hypothetical protein	3.48e-04
32	159	2.6	3591	2	S10236 filamentous hemagglut	1.10e-03
33	159	2.6	3591	2	S21010 filamentous hemagglut	1.10e-03
34	156	2.5	476	2	A41463 alkaline metalloprote	2.19e-03
35	154	2.5	478	2	JN0892 metalloproteinase (EC	3.44e-03
36	152	2.4	449	2	J01277 triacylglycerol lipas	5.39e-03
37	150	2.4	479	2	S26699 alkaline proteinase -	8.43e-03
38	147	2.4	504	2	S12164 metalloproteinase (EC	1.64e-02
39	150	2.4	3016	2	S77300 hypothetical protein	8.43e-03
40	145	2.3	479	2	JN0891 metalloproteinase (EC	2.54e-02
41	137	2.2	1574	1	A38454 myosin MYO2 - yeast (	1.43e-01
42	134	2.2	2035	2	A56088 host cell factor Cl p	2.70e-01
43	133	2.1	550	2	A28166 Kupffer cell receptor	3.32e-01
44	133	2.1	1959	1	A33977 myosin heavy chain, n	3.32e-01
45	133	2.1	2035	2	A40718 host cell factor C1 p	3.32e-01

## ALIGNMENTS

RESULT 1  
ENTRY B30169 #type complete  
TITLE leukotoxin A - Pasteurella haemolytica (serotype 1)  
ALTERNATE\_NAMES lktA protein  
ORGANISM #formal\_name Pasteurella haemolytica  
DATE 12-Oct-1989 #sequence\_revision 15-Nov-1996 #text\_change 05-Sep-1997  
ACCESSIONS B30169; C32051; S29516  
REFERENCE A30169  
#authors Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.  
#journal DNA (1989) 8:15-28  
#title DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.  
#cross-references MUID:89210283  
#accession B30169  
#status not compared with conceptual translation  
#molecule\_type DNA  
#residues 1-953 #label HIG  
REFERENCE A32051  
#authors Strathdee, C.A.; R.Y.C.  
#journal J. Bacteriol. (1989) 171:916-928  
#title Cloning, nucleotide sequence, and characterization of genes encoding the secretion function of the Pasteurella haemolytica leukotoxin determinant.  
#cross-references MUID:89123172  
#accession C32051  
#status not compared with conceptual translation  
#molecule\_type DNA  
#residues 947-953 #label STR  
REFERENCE S29515  
#authors Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.  
#journal Infect. Immun. (1987) 55:1987-1996  
#title Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.  
#accession S29516  
#molecule\_type DNA  
#residues 1-741, 'p', 743-953 #label LOR  
#cross-references EMBL:M20730; NID:g150492; PID:g150494  
COMMENT This organism causes bovine pneumonic pasteurellosis (shipping fever).  
GENETICS  
#gene lktA  
FUNCTION  
#description lyses leukocytes  
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology  
KEYWORDS calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;

```

FEATURE
238-784      #domain hemolysin A homology #label HLXA\
716-807      #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)\
716-724      #region repeat #status atypical\
725-733      #region repeat #status atypical\
734-742      #region repeat\
743-751      #region repeat\
752-760      #region repeat\
761-769      #region repeat\
770-778      #region repeat\
779-787      #region repeat\
790-798      #region repeat\
799-807      #region repeat\
554          #binding_site palmitate (Lys) (covalent) #status
              predicted
SUMMARY      #length 953 #molecular-weight 102044 #checksum 6834
              97.1%; Score 6037; DB 1; Length 953;
Query Match  97.1%; Score 6037; DB 1; Length 953;
Best Local Similarity 97.1%; Pred. No. 0.00e+00;
Matches 913; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 38 KTCAKILYIPQNYQDYDEQNGLDLKAEEELGIEVQREERNNIATAQSLGTIQT 97
Qy 11 KTCAKILYIPQNYQDYDEQNGLDLKAEEELGIEVQREERNNIATAQSLGTIQT 70
Db 98 IGLTERGIVLSAPOIDKLQKTRAGQALSAESIVQNKAKTVLSGIQSLGSLVAGMD 157
Qy 71 IGLTERGIVLSAPOIDKLQKTRAGQALSAESIVQNKAKTVLSGIQSLGSLVAGMD 130
Db 158 LDEALQNNHQALAKAGLELTNSLTENTANSVKTIDEGEQISQFGSKLONIKGLGTIG 217
Qy 131 LDEALQNNHQALAKAGLELTNSLTENTANSVKTIDEGEQISQFGSKLONIKGLGTIG 190
Db 218 DLKLTNGGLDKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELANOVVGNITKA 277
Qy 191 DLKLTNGGLDKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELANOVVGNITKA 250
Db 278 VSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESYAERFKKL 337
Qy 251 VSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESYAERFKKL 310
Db 338 GYDGDNLLEAYQRTGTIDASVTAINALAAIAGGVSAAGSVIASPALLVSGITGVI 397
Qy 311 GYDGDNLLEAYQRTGTIDASVTAINALAAIAGGVSAAGSVIASPALLVSGITGVI 370
Db 398 STILOYSKOAMFEHVANKIHNVKNEKNHKNYPENGYDARYLANLODNKFLNLNK 457
Qy 371 STILOYSKOAMFEHVANKIHNVKNEKNHKNYPENGYDARYLANLODNKFLNLNK 430
Db 458 ELQARVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDAFEEGKHAKDLVQLDSAN 517
Qy 431 ELQARVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDAFEEGKHAKDLVQLDSAN 490
Db 518 GIIDVNSGKAKTQHILFRLPTLTPTGTEHRRVQTKYIYIKLNINRVDSWKITDGAAS 577
Qy 491 GIIDVNSGKAKTQHILFRLPTLTPTGTEHRRVQTKYIYIKLNINRVDSWKITDGAAS 550
Db 578 STFDLNVVQRIEGLDNAGNVTKTKETKIIAKLGLGDDNVFVSGTTEIDGEGYDRVH 637
Qy 551 STFDLNVVQRIEGLDNAGNVTKTKETKIIAKLGLGDDNVFVSGTTEIDGEGYDRVH 610
Db 638 YSRGNYGALTIDATKETECSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 697
Qy 611 YSRGNYGALTIDATKETECSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 670
Db 698 HHAGYTKDTLKAVEEIIQTSNDHIDFKSGFNDAFNGGVDVTIYNDGNDRLFGGKGD 757
Qy 671 HHAGYTKDTLKAVEEIIQTSNDHIDFKSGFNDAFNGGVDVTIYNDGNDRLFGGKGD 730
Db 758 ILDGGNGDDFIDGGKGNLHLGGKGGDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDIT 817
Qy 731 ILDGGNGDDFIDGGKGNLHLGGKGGDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDIT 790

tandem repeat

Db 818 FEKVHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEIIGQNGERITSKOV 877
Qy 791 FEKVHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEIIGQNGERITSKOV 850
Db 878 DDLIAKGNGKITQDELKSVVDVYELLKSKNVTNSLDKLISSVSFTSSNDSRNVLVAPT 937
Qy 851 DDLIAKGNGKITQDELKSVVDVYELLKSKNVTNSLDKLISSVSFTSSNDSRNVLVAPT 910
Db 938 SMLDQSLSLQFARAA 953
Qy 911 SMLDQSLSLQFARGS 926

RESULT 2
ENTRY      A35254      #type complete
TITLE      leukotoxin A - Pasteurella haemolytica (serotype T10)
ALTERNATE_NAMES      lkta protein
ORGANISM      #formal_name Pasteurella haemolytica
DATE      10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change
              05-Sep-1997
ACCESSIONS      S37145; A35254; S34237; S34235
REFERENCE      #authors      Lainson, A.F.; Aitchison, K.; Donachie, W.
              #submission      submitted to the EMBL Data Library, September 1993
              #description      DNA sequence of the leukotoxin A gene from P. haemolytica T10
              #accession      S37145
              #molecule_type      DNA
              #residues      1-955 #label LA1
              #cross-references      EMBL:226247; PID:g400425
REFERENCE      A35254
              #authors      Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
              #journal      J. Bacteriol. (1990) 172:2343-2350
              #title      Secretion and expression of the Pasteurella haemolytica
              leukotoxin.
              #cross-references      MUID:90236888
              #accession      A35254
              #status      preliminary
              #molecule_type      DNA
              #residues      950-955 #label HIG
              #cross-references      GB:M24197; GB:M34943; GB:M34944
REFERENCE      S34235
              #authors      Lainson, A.F.; Aitchison, K.D.; Donachie, W.
              #submission      submitted to the EMBL Data Library, June 1993
              #description      DNA sequence of the carboxy terminal end of leukotoxin A from
              the T3 serotype of Pasteurella haemolytica.
              #accession      S34237
              #molecule_type      DNA
              #residues      745-955 #label LA2
              #cross-references      EMBL:22884; PID:g311829
              #experimental_source      serotype T3
              #accession      S34235
              #molecule_type      DNA
              #residues      723-955 #label LA3
              #cross-references      EMBL:22887; NID:g311824; PID:g311825
              #experimental_source      serotype T10
FUNCTION      attacks cell membranes and causes cell lysis
CLASSIFICATION      #superfamily hemolysin A; hemolysin A homology
KEYWORDS      calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
              tandem repeat
FEATURE
240-786      #domain hemolysin A homology #label HLXA\
718-809      #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)\
718-726      #region repeat\
727-735      #region repeat\
736-744      #region repeat\
745-753      #region repeat\
754-762      #region repeat\
763-771      #region repeat\
772-780      #region repeat\
781-789      #region repeat\

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792-800      #region repeat\
801-809      #region repeat\
556          #binding_site palmitate (Lys) (covalent) #status
SUMMARY      #length 955 #molecular-weight 102187 #checksum 4735
Query Match   88.6%; Score 5510; DB 1; Length 955;
Best Local Similarity 88.4%; Pred. No. 0.00e+00;
Matches 810; Conservative 60; Mismatches 46; Indels 0; Gaps 0;

Db 40 KNGAKIILYIPKDYKSGNGQLDLVKAEEGLGIEVQKEGNDIAKAQTSLSGTONV 99
QY 11 KTGAKIILYIPQNYQDTEQNGQLDLVKAEEGLGIEVQREERNIATAQTSLSGTO 70
Db 100 LGLTERGIVLSAPQDKLLQKNVQALGSSESTAQNTSVLSGVQGNRTVLGMD 159
QY 71 IGLTERGIVLSAPQDKLLQKNVQALGSSESTAQNTSVLSGVQGNRTVLGMD 130
Db 160 LDEALQNESDQLTLAKAGLELNSLIENANSVOTLDAFSEQISQFSGKLQNVKGLGAL 219
QY 131 LDEALQNNENHALAKAGLELNSLIENANSVKTLDGEGDQISQFSGKLQNIKGLTIG 190
Db 220 DLKKNIGGLDKAGLDGIVKSRLLSGATAALVLDADAKTAKVAGFELANQVGNITKA 279
QY 191 DLKKNIGGLDKAGLDGIVKSRLLSGATAALVLDADAKTAKVAGFELANQVGNITKA 250
Db 280 VSSYILAQVAAAGLSTGTPVAAALIASTVAIAPISPLFAGIADKFDRAKSLENYAFKKL 339
QY 251 VSSYILAQVAAAGLSTGTPVAAALIASTVAIAPISPLFAGIADKFDRAKSLENYAFKKL 310
Db 340 GYEGDSLAEOYHGTGTIDASTVNTALAAATAGVSAAGSVASPTALLVSGITGVI 399
QY 311 GYEGDSLAEOYHGTGTIDASTVNTALAAATAGVSAAGSVASPTALLVSGITGVI 370
Db 400 STILOYSKQAMFEHVANKIHNKIVWEKNKGKNTFENGVDARYLANLDQNMKFLNLNK 459
QY 371 STILOYSKQAMFEHVANKIHNKIVWEKNKGKNTFENGVDARYLANLDQNMKFLNLNK 430
Db 460 ELQAEVIAITQQQWDSNTGDLGASIRLGEKVLKSKAYVDAFEQGHKADKLVLQDSAK 519
QY 431 ELQAEVIAITQQQWDSNTGDLGASIRLGEKVLKSKAYVDAFEQGHKADKLVLQDSAN 490
Db 520 GIIDVTNTGEAKTOHLFTPTLLTPTGTEKREVRVQKGYEYITKLNINRVDSWQIKDGAAS 579
QY 491 GIIDVTNTGEAKTOHLFTPTLLTPTGTEKREVRVQKGYEYITKLNINRVDSWQIKDGAAS 550
Db 580 STFDLTNNVQRIQVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDGEGYDRVH 639
QY 551 STFDLTNNVQRIQVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDGEGYDRVH 610
Db 640 YSRGNYGALTIDATKETECSYTVNRVFSKALHEGTSHTTALYGNREKIEYRHSNQ 699
QY 611 YSRGNYGALTIDATKETECSYTVNRVFSKALHEGTSHTTALYGNREKIEYRHSNQ 670
Db 700 HHAGYTKDTLKAVEEIICTSHNDIFKSGFNDAFNGGVDVTIDGNDGNRLFQKGGDD 759
QY 671 HHAGYTKDTLKAVEEIICTSHNDIFKSGFNDAFNGGVDVTIDGNDGNRLFQKGGDD 730
Db 760 IIDGGNGDDFIDGGKNDLHLGGKGGDDIFVHRGGDNDISITSEGNDKLSFSDSNLKDIT 819
QY 731 IIDGGNGDDFIDGGKNDLHLGGKGGDDIFVHRGGDNDISITSEGNDKLSFSDSNLKDIT 790
Db 820 FEKVNHLVITNTKQEKVTVIQRWFAEFAKTQNTVATRDDEKIEIIGQGERITSKQV 879
QY 791 FEKVNHLVITNTKQEKVTVIQRWFAEFAKTQNTVATRDDEKIEIIGQGERITSKQV 850
Db 880 DELIEKNGKIAQSELTQVVDNQLLKYGRDASNSLDKLISSAFTSSNDSRNVLASPT 939
QY 851 DDLIAKNGKITQDELKSKVVDNVELLKHKNVTNSLDKLISSAFTSSNDSRNVLASPT 910
Db 940 SMLDPSLSSIOFARAA 955
QY 911 SMLDPSLSSIOFARAA 926
```

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RESULT 3
ENTRY
TITLE toxin II - Actinobacillus pleuropneumoniae
ALTERNATE_NAMES cytolysin II: RTX-toxin II (ApXII)
ORGANISM #formal_name Actinobacillus pleuropneumoniae
DATE 09-Mar-1990 #sequence_revision 01-Nov-1996 #text_change
06-Dec-1996
ACCESSIONS B33389; S18853; B43599
REFERENCE A33389
#authors Chang, Y.F.; Young, R.; Struck, D.K.
#journal DNA (1989) 8:635-647.
#title Cloning and characterization of a hemolysin gene from
#cross-references MUID:90126233 Actinobacillus (Haemophilus) pleuropneumoniae.
#accession B33389
#molecule_type DNA
#residues 1-956 #label CHA
#cross-references GB:M30602; PID:g141825
#experimental_source serotype 5
REFERENCE S18852
#authors Smits, M.A.; Briare, J.; Jansen, R.; Smith, H.E.; Kamp,
E.M.; Gielkens, A.L.J.
#submission submitted to the EMBL Data Library, July 1991
#description Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
#accession S18852
#molecule_type DNA
#residues 1-956 #label SM1
#cross-references EMBL:X61111; PID:g38941
REFERENCE A43599
#authors Smits, M.A.; Briare, J.; Jansen, R.; Smith, H.E.; Kamp,
E.M.; Gielkens, A.L.J.
#journal Infect. Immun. (1991) 59:4497-4504
#title Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
#cross-references MUID:92040145
#accession B43599
#status preliminary
#molecule_type DNA
#residues 1-27:948-956 #label SM2
#cross-references GB:X61111
COMMENT This organism causes porcine pleuropneumonia.
GENETICS apxIIA; apxA; clyIIA
FUNCTION attacks blood cell membranes and causes cell lysis
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology
KEYWORDS calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
tandem repeat
FEATURE
243-787 #domain hemolysin A homology #label HLVA\
719-801 #region 9-residue repeats\
719-727 #region repeat #status atypical\
728-736 #region repeat #status atypical\
737-745 #region repeat\
746-754 #region repeat\
755-763 #region repeat\
764-772 #region repeat\
773-781 #region repeat\
782-790 #region repeat\
793-801 #region repeat\
557 #binding_site palmitate (Lys) (covalent) #status
predicted
SUMMARY #length 956 #molecular-weight 102531 #checksum 5232
Query Match 68.4%; Score 4254; DB 1; Length 956;
Best Local Similarity 67.1%; Pred. No. 0.00e+00;
Matches 615; Conservative 155; Mismatches 139; Indels 8; Gaps 7;
Db 45 GAKKILYIPQY--DSGGNGVQDLVKAANDLGIETVREERSNLDIAKTSFDTTQKILG 102
QY 13 GAKKILYIPQYQYDTEQNGQLDLVKAEEGLGIEVQREERNIATAQTSLSGTTAIG 72
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Db 641 YSRGEYCALVIDATAETKSGYSVKRYVGDASKALHETIATHQINVGNGREEKIEYRREDDR 700
QY 611 YSRGNYGALTIDATKTEQSGSYTVNRVETGKALHEVTHSTHALVNGREEKIEYRHSNNQ 670
Db 701 FHTGYTVDLSKSVEEIIGSFQDFDVFHGGNGVDITDGNDDHFLFGGAGDD 760
QY 671 HHAGYTKDTLKAVEEIIIGTSHNDIFKSGFNDAFNGDGDVDIDGNDNRFLFGGKDD 730
Db 761 VIDGNGNVLVGTTGNDIISGGKNDIYVHKGTGDNDSITDSGGQDKLAFSDVNLKDLT 820
QY 731 ILDGGNGDDFDGKGNDLLHGGKDDIFVHRKGGDNDIITDSGNDKLSFSDNLKDLT 790
Db 821 FKKVDSLEIINOKGKVRIGNFLEDDLASTVANYKATNDRKIEEIIIGGGERITSEQV 880
QY 791 FEKVHNLVITNSKKEVTIONFREADFAKEVPNYKATKDEKIEEIIIGGGERITSQV 850
Db 881 DKLIKGNNOISAEALSKVNDYNTSKDRONSLSKLSSVSGSFSSDFRNILGTYV 940
QY 851 DDLIAGNGKITODELSKVVDNYELLKHSKNVNSLDKLSSVSAFTSSDSNRVLVA-P 909
Db 941 PSSIDVS-NNIQLARAA 956
QY 910 TSMLDQSLSSLOFARGS 926

RESULT 5
ENTRY #type complete
TITLE toxin III - Actinobacillus pleuropneumoniae (serotype 8)
ALTERNATE_NAMES RTX-toxin III (ApxIIIA)
ORGANISM #formal_name Actinobacillus pleuropneumoniae
DATE 19-Dec-1993 #sequence_revision 01-Nov-1996 #text_change
ACCESSIONS 06-Dec-1996
REFERENCE B49219; S48043; S29958
#authors Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
#journal Infect. Immun. (1993) 61:947-954
#title Cloning and characterization of the Actinobacillus pleuropneumoniae RTX-toxin III (ApxIII) gene.
#cross-references MUID:93162836
#accession B49219
#molecule_type DNA
#residues 1-1052 #label JAN1
#cross-references EMBL:X68815; PID:g38958
#experimental_source strain 405, serotype 8
#note sequence extracted from NCBI backbone (NCBIN:125168, NCBI:P:125170)

REFERENCE S48042
#authors Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.; Smits, M.A.
#journal Infect. Immun. (1994) 62:4411-4418
#title Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (Apx) operons: characterization of the ApxIII operons.
#accession S48043
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-1052 #label JAN2
#cross-references EMBL:X80055; PID:g558152
#experimental_source strain 405, serotype 8
#note the nucleotide sequence was submitted to the EMBL Data Library, July 1994
COMMENT This organism causes porcine pleuropneumonia.
GENETICS
#gene apxIIIA
FUNCTION
#description lyses lung macrophages
#CLASSIFICATION superfamily hemolysin A; hemolysin A homology
KEYWORDS calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat
FEATURE
254-804 #domain hemolysin A homology #label HLYA\

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736-862 #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIFY]-X)\
736-744 #region repeat #status atypical\
745-754 #region repeat #status atypical\
754-762 #region repeat #status atypical\
763-771 #region repeat\
772-780 #region repeat\
781-789 #region repeat\
790-798 #region repeat\
799-807 #region repeat\
808-816 #region repeat\
818-826 #region repeat #status atypical\
827-835 #region repeat\
836-844 #region repeat #status atypical\
845-853 #region repeat\
854-862 #region repeat\
571,702 #binding_site palmitate (Lys) (covalent) #status predicted

SUMMARY #length 1052 #molecular-weight 112809 #checksum 2655
Query Match 42.1%; Score 2616; DB 1; Length 1052;
Best Local Similarity 52.7%; Pred. No. 0.00e+00;
Matches 404; Conservative 178; Mismatches 165; Indels 20; Gaps 17;

Db 55 GNKLVLVIP-K-EYDGSVGNFEDLVKAAEELGIQYKYNRNELEVAHKSLSGTADQFLGL 112
QY 14 AKKIILYIPONTQYDTEQNGQDLVKAABEELGIEVQREERNNTAQTSLGTQTAIGL 73
Db 113 TERGLTFLAPQLDQFLQKHSKISNVVSGSTGDVASKLAKSQTIIISQISVLGTLAGINL 172
QY 74 TERGIVLSAPOIDKLLQK-TKAGQALGSRAES-IVQNAKAKTVLSQISVLSGLAGMDL 131
Db 173 NEAIISSGSELEAEAGVSLASELVSNIAKGTITIDAFDTQIQNFQKLVENAKLGGVGR 232
QY 132 DEALONNSNOHALAKAGLELTNSLIENIANSVKTLDFEGEIQISQKLNKIKGLTGLD 191
Db 233 OLONISGSALSKTGLGLDIISLLSGVTASFALANKNASTSKVAAGFELSNOVIGITK 292
QY 192 KLNIGG--LDKAGLGLDVISLLSGATLAALVADNASTAKKVGAGFELANOVGNITK 249
Db 293 AVSSYILAQRALAGLSTTGPAAALIASISLAIPLAFNRVADFNKRSKEIGFAERFKK 352
QY 250 AVSSYILAQRVAAGLSTTGPVAALIASTVLSLAISPLAFAGIADKFHAKSLESYAEFRK 309
Db 353 LGYDGLKLLSEFYHEAGTIDASTITISTALSAIAGTAASAGALYCAPITLLVITGTL 412
QY 310 LGYDGNLLAEYQRGTTIDASTVTAINTALAAIAGGVSAAAGSVIAPALLVSGITGV 369
Db 413 ISGILEFSQPMLDHVASKIGNKIDWEKK-YGKNYFENGYDARHKAFLSDSFLSSFN 471
QY 370 ISTILOYSKOAMFERVANKIHNVKIVEMKNNHGNKYNFENGIDARYLANLQDNKKFLNLN 429
Db 472 KOYETERAVLITOORWDEYIGELAGITGDKLSSGKAYVDYFOEKKLLEKKPDDFSKV 531
QY 430 KELQAEVTAITQQQNDNIGDLAGISRGKVKLSKAYVDAAFEKHHI--KADKL--VQ 485
Db 532 FDPTEKIDISNS-QTSTL-LKFVTPLLTPGTESRERTOTGKYEYITKLVKGKQWVN 589
QY 486 LDSANGIIDVNSGKAKTQHILFRTPLLPTEHREVQTKVEYITKLNINRVDSKMIT 545
Db 590 GVXDKGAVDYTNLIQAHIS-SSVARGEYREVRLVSHLGNQNDKVFLAAGSAEIHAGE 648
QY 546 DGAA--STFDLTNVVORIGIELDNAGNVTKTKETKIAKLGEGDDNVFVSGGTTEIDGG 604
Db 649 GHVDVYDKTDGTLVLDGTGKATEQGRYSVTRLSGATKILREVINKQKSAVKREETLE 708
QY 605 GYDRVHYSRNGYALTDATKETEQQSYTVNR-FVETGRALHEVTTHTALVNGREEKIE 663
Db 709 YRDYELTQSGNSNLKAHDELHVSVEEIIIGNSQNDREFKSRFDIFHGADGDDLLGNDGDD 768
QY 664 YRHSN-NQH-HAGYTKDTLKAVEEIIIGTSHNDIFKSGFNDAFNGDGDVDITDGNND 721
Db 769 ILYDGNDELRGDNGNDQLYGEGGNDKLLGGNGNN-YL-SGGDGNND 813

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QY 722 RLFGGKDDILDGGNGDDFDGKGKNDLLHGGKDDIFVHRKGDGND 768

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RESULT 6
ENTRY   S51784      #type complete
TITLE   toxin III - Actinobacillus pleuropneumoniae (serotype 2)
ALTERNATE_NAMES  RTX-toxin IIIA (ApXIIIA)
ORGANISM #formal_name Actinobacillus pleuropneumoniae
DATE     14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change
        06-Dec-1996
ACCESSIONS S51784
REFERENCE  S51783
#authors   Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.
#journal   DNA Cell Biol. (1993) 12:351-362
#title     Molecular analysis of the Actinobacillus pleuropneumoniae RTX
           toxin-III gene cluster.
#accession S51784
#status    preliminary
#molecule_type DNA
#residues  1-1049 ##label CHA
##cross-references EMBL:L12145; FID:g470685
COMMENT   This organism causes porcine pleuropneumonia.
GENETICS
#gene      apXIIIA
FUNCTION
#description lysates lung macrophages
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology
KEYWORDS      calcium binding; cytolysis; exotoxin; lipoprotein; tandem
           repeat
FEATURE
254-803    #domain hemolysin A homology #label HLXN
735-861    #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)\
735-743    #region repeat #status atypical\
744-753    #region repeat #status atypical\
753-761    #region repeat
762-770    #region repeat
771-779    #region repeat
780-788    #region repeat
789-797    #region repeat
798-806    #region repeat
807-815    #region repeat #status atypical\
817-825    #region repeat
826-834    #region repeat
835-843    #region repeat
844-852    #region repeat
853-861    #region repeat
571,702    #binding_site palmitate (Lys) (covalent) #status
           predicted
SUMMARY    #length 1049 #molecular-weight 112491 #checksum 8565

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Query Match 41.3%; Score 2566; DB 1; Length 1049;
Best Local Similarity 52.2%; Pred. No. 0.00e+00;
Matches 401; Conservative 177; Mismatches 167; Indels 23; Gaps 20;

Db 55 GNKLVLVIP-K-EYDGSVNGFEDLVKAAEELGIVQVYRNLEVAHSLGTAQDFGL 112
QY 14 AKRIILIFQNTQYDTEQNGQDLVKAABELGIEVQREERNIAQTSLSLTQIATGL 73
Db 113 TERGLTFLAPQLDQFLQKHSKISNVVSGSTGDAVSKLAKSQRIISQISVLGTLAGINL 172
QY 74 TERGIVLSAPQIDKLLQK-TKAQALGSAES-IVQNANKAKTVLSQISVLGSLAGMDL 131
Db 173 NEAITSGGSELEAEAGVSLAELVSNIAKGTITDAFTQTQINFG-KLAENAKGLGGVG 231
QY 132 DEALQNNNQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL-QNIKGLGTIG 190
Db 232 ROLQNTSSGALSKTGGLDIISSLSGSVTRSFALRNKNASTTKVAAGFELSNOVIGGIT 291
QY 191 DKLKNIGG--LDKAGLGLDVISGLLSGATVLAALVLADKNASTAKKVGAGFELANQVGNIT 248
Db 292 KAVSSYILAQRLRAGLSTTGPAALIASISLAISPLAFRLVADNFRNSKEIGEFARFK 351
QY 249 KAVSSYILAQRAAGLSSTGPAALIASISLAISPLAFAGIADKNFAKSLAESIAERFK 308

```

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Db 352 KLGYDGDKLLSEFYHEAGTIDASITTIISTALSAAGTAAASAGALVCAPITLLVTGITG 411
QY 309 KLGYDGDNLLAEYQRTGTIDASTVAINTAALAAAGSVAAAGSVIAPIALLVSGITG 368
Db 412 LISGLEFSKPMIDHVASKIGNKIDWEKK-YGNKYFENGYDARHKAFLDEFSLSLSF 470
QY 369 VISTLIQISKAMFEHVANKIHNKIVWEKNNHKNYFENGYDARYLANQDNKKFLNL 428
Db 471 NKQYTERAVLITQORWDEYIGELAGITGKGDKLSSGRAYVDYFOEGKLLKPKPDFSKV 530
QY 429 NKELQAERVAITQQQWNNIGDLAGISRLGEKVLGRAYVDAFEKGHI--KADKL--V 484
Db 531 VDPPTKGEIDISNS-OTSTL-LKFVTPLLTPTGTSRERTQTGKYEYITKLVKGDKWV 588
QY 485 QLDSSANGIIVSNCGKAKTQILFTPLLTPTGTEHREVRVOTGKYEYITKLINRVDSWKI 544
Db 589 NGVKDKGAVDYTNLIQAHIS-SSVARGEYREYRLVSHLGNKNDKVFLLAAGSAEIHAG 647
QY 545 TDGAA-SSTFDLTNNVQIRIGIELDNAGNVTKETKIILAKIGEGDNNVFGSGTTEIDGG 603
Db 648 EGHVYVYDKTDGTLIVIDGKATEQGRYSVTRLSGATKILREVKNQKAVGKREETL 707
QY 604 EGYDRVHYSRNGYALTIDATKETEQGSYTVNR-FVETGKALHEVTSHTHALVGNREKI 662
Db 708 EYRDYELTQSGNSNLKAHDELHVSVEEI-GSNORDEFKSGKFRDIFHGADGDDLLNGNDG 766
QY 663 EYRHSN-NQH-HAGYTTKDTLKAVEEIIIGTSHNDIFKSGKFNDAFNGGVDVTIDGNDGN 720
Db 767 DILYDKGNDLGRGNDOLYGGEGDDKLLGGGNN-YL-SGGDGDND 812
QY 721 DRLFQGGKDDILDGGNGDDFDGKGKNDLLHGGKDDIFVHRKGDGND 768

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RESULT 7
ENTRY   LEECA      #type complete
TITLE   hemolysin A - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE     30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change
        20-Mar-1998
ACCESSIONS A24433; I41280
REFERENCE  A24433
#authors   Felmlee, T.; Pellett, S.; Welch, R.A.
#journal   J. Bacteriol. (1985) 163:94-105
#title     Nucleotide sequence of an Escherichia coli chromosomal
           hemolysin.
#cross-references MUID:85234404
#accession A24433
#molecule_type DNA
#residues  1-1023 #label FEL
##cross-references GB:M10133; GB:M12863; NID:g146377; PID:g146379
#experimental_source strain J96, O4 serotype
REFERENCE  A55387
#authors   Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.
#journal   Science (1994) 266:1992-1996
#title     Fatty acylation of two internal lysine residues required for
           the toxic activity of Escherichia coli hemolysin.
#contents  annotation; lysine palmitoylation
#note      lysine modification is performed by the hlyC gene product
REFERENCE  I41280
#authors   Haertlein, M.; Schiessl, S.; Wagner, W.; Rdest, U.; Kreft,
           J.; Goebel, W.
#journal   J. Cell Biol. (1983) 22:87-97
#title     Transport of hemolysin by Escherichia coli.
#accession I41280
#status    translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  1,T',3,V',5,T',7-44 #label RES
##cross-references GB:M29173; NID:g146337; PID:g146338
GENETICS
#gene      hlyA
#description attacks blood cell membranes and causes cell lysis

```





Qy 540 DSWKITDGA--SSTEDLTNVQIGIELDNAGNVTKTKETKIIAKLGGEDDNNVFGSGTT 598

Db 631 NIYACKGHVYVYKTDITGTLTIDGTTKATEAGNYTVTRVLGDGVKVLQEVVKEQEVSVGK 690

Qy 599 EIDGEGYDRVHYSRGNYGALTIDATKETQGSYTVNRFVETG-KALHEVSTHTALVGN 657

Db 691 RTEKTOYSYERTHINGNLNTETNLNYSVEELIGTTRADKPFSGKFTDIFHCAGDDLLIE 750

Qy 658 REEKIEYRHSNNQHAG--YVT-KDTLKAVEELIGTSHNDIFKGSFNDFAFNGGDDVDFID 715

Db 751 GNDGNDRLYGGKNDTLGGGNDGDDOLYGGGNDKLGIVAGNN--YLN--GGDGD 801

Qy 716 GNDGNDRLFGKGGDDILDGGNGDDFIDGGKGNDDLHGGKGGDDIFVHRKGGDND 768

RESULT 9

ENTRY #type complete

TITLE hemolysin - Escherichia coli

ORGANISM #formal\_name Escherichia coli

DATE 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 23-Apr-1997

ACCESSIONS I41078

REFERENCE I41078

#authors Schmidt, H.; Beutin, L.; Karch, H.

#journal Infect. Immun. (1995) 63:1055-1061

#title Molecular analysis of the plasmid-encoded hemolysin of Escherichia coli O157:H7 strain EDL 933.

#cross-references MUID:95172699

#accession I41078

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type DNA

#residues\_type 1-998 #label RES

#cross-references EMBL:X79839; NID:g860924; PID:g860925

CLASSIFICATION #superfamily hemolysin A; hemolysin A homology

FEATURE

233-776 #domain hemolysin A homology #label HLVA

SUMMARY #length 998 #molecular\_weight 107058 #checksum 125

Query Match 37.3%; Score 2321; DB 2; Length 998;

Best Local Similarity 46.8%; Pred. No. 4.17e-299;

Matches 367; Conservative 200; Mismatches 188; Indels 29; Gaps 23;

Db 29 RSAGKLLILPDNY--EA-QGVGINELVKADELGIETRIERTDRTAIAQFTGAEEKV 85

Qy 11 KIGAKILYIPONTQYDETGNGLDLVKAAEELIEVQRENNIATQTSLTQTA 70

Db 86 VGLTERGVAIFAPQDKLQRYKQYKIGGTAENVGNLKGAGTVLSALONFTGIALSG 145

Qy 71 IGLTERGIVLSAPQDKLQK-TRAGQALG-SAESIVQANKAKTVLSGIIQSLVLAG 128

Db 146 MALDELLRKQREGEDISNDIAKSSIELINQIVDTVSSINTVSFSQLNQLGSFLSSK 205

Qy 129 MDLDEAL--QNNNS-N--QHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFSGKLQNI 183

Db 206 PRLSSVGKLNLPDLGPGDGLVSVGILSAVSASFILGNSDAHTGTAKAAGIELTQV 265

Qy 184 KGLGTGLDKLKNIGGLDKAGLGLDVISLLSGATAALVLADKNASTAKKVGAGFELANQV 243

Db 266 LGNVKAYSQVILAQMAQGLSTTAASAGLITSAYMLAISPLSFIAAADKFERAKQLESY 325

Qy 244 VGNITKAVSSYILAQVAAGLSSTGTPVAALTAFTVSLAISPLAFAGIADKFNHAKSLESY 303

Db 326 SERPKLNYEGDALLAGPHKGTGAIDAGLTINTVLLSVSSAGVSAASASLIGAPISMLV 385

Qy 304 AERFKKLYGDGNDLAEYQRTGTIDASVTAINALAAAGVSAASAGSVIASPILLV 363

Db 386 SALTGTSSILEASKQAMFEHVAEKFAARINEWEKE-HGKNYFENGYDARHAAFLEDSLS 444

Qy 364 SGITGVISTIQQSKQAMFEHVAEKFAARINEWEKE-HGKNYFENGYDARHAALQDNMK 423

Db 445 LLADFSGHAYERVAITHQWDEKIGELAGITRNADRSQSGKPYNYLNGGLLEAQPK 504

Qy 424 FLNLNKLQEAERVTAITQQQWNNIGDLAISRLGERKVLGSKAYVDFAFEGSKIKAD-K 482

Db 505 EFTQOVEDPQGTIDLS-TGNVSSV-LTFITPTTPGEEVRRKQSKGYEYMTSLIYNGK 562

Qy 483 -LVQ--LDSANGIIDVSNKAKTQHLFTPLTPTGTEHRRVQTGKYEYITKLINRV 539

Db 563 DTWSVKGIKNHKGYDYDKLIO-F-VE--K--N-TKHQARIISSELGDKDDVYSGAGSS 615

Qy 540 DSWKITD-GAASSTFDLTNVQVIGIELDNAGNVTKTKETKIIAKLGGEDDNNVFGSGTT 598

Db 616 EVFAGEGYDPVSYNKTDVGLTIDATGAPKPEGYIVPKNMYGDVEVLQEVVKEQEVSVGK 675

Qy 599 EIDGEGYDRVHYSRGNYGALTIDATKETQGSYTVNRFV-ETCKALHEVSTHTALVGN 657

Db 676 RTEKIQTRDFEFTGGIPDYVIDNLHSVEELIGKHDEFGKGFNDIFHCAGDNDYIEG 735

Qy 658 REEKIEYRHSNNQHA--GYTTKDTLKAVEELIGTSHNDIFKGSFNDFAFNGGDDVDFID 716

Db 736 NYGNDRLYGGDGDYISGGGDDOLFGSGNDKLSGGDGN--YL-TGSGNDELQAHGAY 793

Qy 717 NDGNDRLFGKGGDDILDGGNGDDFIDGGKGNDDLHGGKGGDDIFVHRKGGDNDIITSDGN 776

Db 794 NILS 797

Qy 777 DKLS 780

RESULT 10

ENTRY #type complete

TITLE RTX-toxin I - Actinobacillus pleuropneumoniae

ALTERNATE\_NAMES hemolysin ApxI

ORGANISM #formal\_name Actinobacillus pleuropneumoniae

DATE 19-Jul-1996 #sequence\_revision 08-Nov-1996 #text\_change 11-Apr-1997

ACCESSIONS I39643; S18769; I39645; S60732; S35781

REFERENCE I39641

#authors Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.

#journal Infect. Immun. (1993) 61:3688-3695

#title Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI) operon.

#cross-references MUID:93366425

#accession I39643

#status nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ

#molecule\_type DNA

#residues 1-1022 #label RES

#cross-references EMBL:X73117; NID:g312897; PID:g312899

REFERENCE S18769

#authors Frey, J.; Meier, R.; Gygi, D.; Nicolet, J.

#journal Infect. Immun. (1991) 59:3026-3032

#title Nucleotide sequence of the hemolysin I gene from Actinobacillus pleuropneumoniae.

#cross-references MUID:91348845

#accession S18769

#status preliminary

#molecule\_type DNA

#residues 1-209, 'AMPVLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 #label FRE

#cross-references EMBL:X52899; NID:g38949; PID:g38950

REFERENCE I39644

#authors Frey, J.; Haidemann, A.; Nicolet, J.; Boffini, A.; Prentki, P.

#journal Gene (1994) 142:97-102

#title Sequence analysis and transcription of the apxI operon (hemolysin I) from Actinobacillus pleuropneumoniae.

#cross-references MUID:94237497

#accession I39645

#status nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ

#molecule\_type DNA

#residues 1-209, 'AMPVLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 #label RE2

#cross-references EMBL:X68595; NID:g505568; PID:g505570

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REFERENCE
#authors
#journal
#title
#accession
#status
#molecule_type
#residues
COMMENT: This organism causes porcine pleuropneumonia.
GENETICS
#gene
#description
#classification
#keywords
FEATURE
243-789
721-847
721-729
730-738
739-747
748-756
757-765
766-774
775-783
784-792
793-801
812-820
821-829
830-838
839-847
560,686
SUMMARY
Query Match 36.9%; Score 2291; DB 1; Length 1022;
Best Local Similarity 46.2%; Pred. No. 7,96e-295;
Matches 376; Conservative 201; Mismatches 206; Indels 31; Gaps 26;

Db 39 KQAGKILYIPKDYQAST--GSSLDLVKAAEALGIEVHRSEKNGTALAKELFGITEKL 96
QY 11 KTGAKKILYIPQNYQDTFGNGLDLVKAAEELGIEVQREERNNTAQTSLGTIQT 70
Db 97 LGSERGIALFAPQDKLLNKNKLSLGSSEALGQRLNKTOTALSALQSLGTAIG 156
QY 71 IGLTERGIVLSAQIDKLLQKT-KAGALG-SAESIVQNKAKATVLSGTSILGSLVAG 128
Db 157 MDLDSLLRRRNGEDVSGSELAKAGVDLAALQVDNTASATGTVDFAEQLGKLGNALSN 216
QY 129 MDLDEALQNNNS-QH---A-LAKAGLELTNSLTENIANSVKTLDFEGEQISQFGSKLQNI 183
Db 217 R-LSGLASKLNLPDLISLACGPDVAGSIIISVVSASFILSNKNDADAGTKAAAGIEISTKI 275
QY 184 KGLGTGLDKLKNKGGLDKAGLDLVISGLSGATLAALVLADKNASTAKKYAGAGFELANQV 243
Db 276 LGNIGKAVSYIIAQRVAAGLSITTAATGGTIGSVVLAISPLSFLNVADRFERAKOLEQY 335
QY 244 VGNITKAVSYIIAQRVAAGLSITGPVVAIIASTVLSAISPFAFAGIADRFNKALESY 303
Db 336 SERFKFEGEDSLLASFYRETGAIEAALTINSVLSSAASAGVGAATGSLVGAPVAALV 395
QY 304 AERFKKLGVDGNLLAEYQRTGTIDASVTAINTALAAIAGSVSAAAAGSVIASPIALLV 363
Db 396 SAITGIISGLIDSKQAIFERVATKANKIDWEKK-HGKNYFENGVDARHSAPLEDTFE 454
QY 364 SGITGVISTILOYSKQAMFHFVANKIHNKIVEKNHNGKNYFENGVDARYLANLQDNMK 423
Db 455 LLSQYNKEYSVERVAITQORWDVNIAGITRKSGSDTKSGKAYVDFFEGLLEKEPD 514

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QY 424 FLNLNKLQAEARVIAITQQQWNNIGDLAGISRLGKVLGSKAYVDAFEEGKHI-K-AD 481
Db 515 RDKKVFDPLEGGKIDLSSINKT-TL-LKFVTPVFTAGEIRERKQKQKGYEYWTLEFVK 572
QY 482 KLVQ--LDSANGIIDVNSGKRAKTHILPRLPTGTEHREVRQTKYEYITKLINRV 539
Db 573 EKVVVTGVQSHNAIYDTNLIQ-LAID-RK-GE-K-RQVTTIESHLGKENDRIYLSGSS 626
QY 540 DSKWITDGA--STFDLTNVVORIGIELDNAGNVTKETKIILAKGEGDDNVFVSGIT 598
Db 627 IYVAGNGHDVAYYDKTDGTLGTFDQSAQAKAGEYIIVTKELKADVKVLKVVKTQDISV 686
QY 599 EIDGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETG-KALHEVTSHTALVN 657
Db 687 RSEKLEYRDEYELSPFELNGIRAKDELHVSVEELIGSNRDKKFFGSRFTDIFHGAKGDEI 746
QY 658 REEKIEYRSHN-NQHHAGY-Y-TKDTLKAVEELIGTSHNDIFKSGKFNDAFNGGVDTI 714
Db 747 YGNDGHDILYDGDNDVIVHGGDNDHLVGGNDRLIGGKGN-FLN-GDGDDELQVFE 804
QY 715 DGNNDGNDRLFGGKDDILDGGGDDFDIDGKGNLDLHGKGGDIFVHRKGDGNDITDSD 774
Db 805 GQYNVLGAG-NDILYSGDGTNLFDGVGNDKI 837
QY 775 GNDKLSFSDSNLKDITFEKVKHNLVITNSKKEV 808

RESULT 11
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references
#molecule_type
#residues
#note
REFERENCE
#authors
#journal
#title
#accession
#status
#molecule_type
#residues
#note
REFERENCE
#authors
#journal
#title
#accession
#status
#molecule_type
#residues
#note

A37205 #type complete
leukotoxin A - Actinobacillus actinomycetemcomitans
#formal_name Actinobacillus actinomycetemcomitans
16-Sep-1992 #sequence_revision 01-Nov-1996 #text_change
06-Dec-1996
A37205; A60768; B34345; A32276; PH0267; PH0266; S17284
Kraig, E.; Dailey, T.; Kolodrubetz, D.
Infect. Immun. (1990) 58:920-929
Nucleotide sequence of the leukotoxin gene from
Actinobacillus actinomycetemcomitans: homology to the
alpha-hemolysin/leukotoxin gene family.
#cross-references MUID:90202154
#accession A37205
#molecule_type DNA
#residues 1-1055
#label KRA
#cross-references GB:X16829; PID:g38645
#note the authors present evidence that the nucleotide
sequence is correct in the vicinity of amino acid 926;
the sequence B34345 differs after this residue as a
result of a frameshift from one missing nucleotide

A60768
Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraig, E.
Infect. Immun. (1989) 57:1465-1469
Cloning and expression of the leukotoxin gene from
Actinobacillus actinomycetemcomitans.
A60768
nucleic acid sequence not shown; not compared with
conceptual translation
#molecule_type DNA
#residues 297-309, 'Y', 311-364; 434-440, 'KC', 443-474, 'H', 476-489,
's', 491-493, 'VLK', 497-498 #label KOL
#note this preliminary sequence has been revised in reference
A37205
A34345
Lally, E.T.; Golub, E.E.; Kieba, I.R.; Taichman, N.S.;
Rosenbloom, J.; Rosenbloom, J.C.; Gibson, C.W.; Demuth,
D.R.
J. Biol. Chem. (1989) 264:15451-15456
Analysis of the Actinobacillus actinomycetemcomitans
leukotoxin gene. Delineation of unique features and
comparison to homologous toxins.
#cross-references MUID:89359382
#accession B34345
#molecule_type DNA

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##residues      1-239,'Y',241-259,'H',261-335,'A',337-415,'S',417-438,
                  'S',440-723,'N',725-926,
                  'VHDKRLHSYSEVSTNHSIKRLKSLVKMGSGLLRKLTLIFLIR',
                  'VGTQRQLHSLPDLRIKVSQVALCLLVRQVCLHRKSPVQCMILVVLFOOPY
                  VLHV', 'PVKRYPLRCHRPITLTLQIR' ##label LAL
##cross-references GB:M27933
REFERENCE
#authors      Lally, E.T.; Kleba, I.R.; Demuth, D.R.; Rosenbloom, J.;
               Golub, E.E.; Tachman, N.S.; Gibson, C.W.
#journal      Biochem. Biophys. Res. Commun. (1989) 159:256-262
#title        Identification and expression of the Actinobacillus
               actinomycetemcomitans leukotoxin gene.
#cross-references MUID:89165863
#accession    A32276
#status       nucleic acid sequence not shown; not compared with
               conceptual translation
#molecule_type DNA
##residues    430-438,'S',440-476,'R',478-506,'RVRS',511,
               'QSIAINSLNTD',523-541,'I',543,'POV','RKG',556,'A',
               558-589,'MIFY',594-689,'ST',693-723,'N',725-754
               #label LA2
##note        this preliminary sequence has been revised in reference
               A34345
REFERENCE      PH0266
#authors      Ohta, H.; Miyagi, A.; Kato, K.; Fukui, K.
#submission   submitted to JIPID, July 1995
#description   Modulation of leukotoxin production by growth rate and
               bicarbonate in a toxin production-variable strain of
               Actinobacillus actinomycetemcomitans.
#accession    PH0267
#molecule_type protein
##residues    17-42 ##label OHT
##experimental_source strain 301-b
#accession    PH0266
#molecule_type protein
##residues    2-6,'L',8-26 ##label OH2
COMMENT       This organism is implicated in juvenile periodontitis.
GENETICS
#gene         ltxA
FUNCTION
#description   lyses human polymorphonuclear lymphocytes and monocytes
CLASSIFICATION superfamily hemolysin A; hemolysin A homology
KEYWORDS       cytolysis; hemolysis; lipoprotein; periplasmic space; tandem
               repeat
FEATURE
245-790        #domain hemolysin A homology #label HLYA\
731-847        #region 9-residue repeats (G-X-G-[DN]-D-X-[LVIVF]-X)\
731-739        #region repeat #status atypical\
740-748        #region repeat\
749-757        #region repeat\
758-766        #region repeat\
767-775        #region repeat\
776-784        #region repeat\
785-793        #region repeat #status atypical\
794-802        #region repeat\
803-811        #region repeat\
812-820        #region repeat\
821-829        #region repeat\
830-838        #region repeat\
839-847        #region repeat\
562,687        #binding_site palmitate (Lys) (covalent) #status
               predicted
SUMMARY
#length 1055 #molecular-weight 113853 #checksum 7343
Query Match    35.5%; Score 2207; DB 1; Length 1055;
Best Local Similarity 46.1%; Pred. No. 7,59e-283;
Matches 371; Conservative 189; Mismatches 210; Indels 34; Gaps 25;
Db 44 KTG-KKLILYIPKNVK-----KNGTLIAKAAQKIGIEVYHGGKDPALTNGILNTGKGL 98
QY 11 KTGAKKIILYIPONYQYDTEQGNQLDLKAAAEELGIEVQREERNIATQTSLSGTIQT 70
Db 99 LGLTGLTLFAPELDKWIOGNKHLNSVGSTGNLTKAIDKQVSLGLTLQAFINTAFSGM 158

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QY 71 IGLTERGVLSAPQDKLQTKKA-QQALGSAESIVQNNRAKTVLSIQISLGSVLGAM 129
Db 159 DLDALIKARQGNKNTVDQLAKASLNLINELIGTISSTNNVDTFSKQNLKLGALGOVK 218
QY 130 DLDEAL--QNNNS-QHA-LAKAGLELNSLIENIANSVKTLDEGEQISOFGSKLQNIK 184
Db 219 HFSFGDKLKLPLKGNLKGKLGALSGVLSAISALLANKADADATATKAAAELTNKVL 278
QY 185 GLGTGLDKLKNIGGLDKAGLGLDVISGLLSGATAALVADKNASTAKVGVAGFELANOV 244
Db 279 GNIGKAITOYLIAORAAAGLSTTGPVAGLIAVSVLSLSPSLGIAKQFQDPRMLLEYS 338
QY 245 GNITKAVSYILAQRVAAGLSTGPVAAIATVSLASPLAFAGIADKFNHAKSLESIA 304
Db 339 KRFKFGYNGDSLGLQFYKNTGIADAAITTTIVLSAIAAGVGAASAGSLVGAPIGLLVS 398
QY 305 ERFKGLGYDGNLLAEYQRTGTIDASVTAINALAAAGVSAAGSVTASPTALLVS 364
Db 399 AITSLISIGILDASQAVFEHIANQLADKIKAWE-NKYKNTFENGICYDARHSFAFLEDSUKL 457
QY 365 GITGVISTILQYSQAMPFHVANKIHNNKIVWEKNHNGKNTFENGICYDARYLANLDQNMKE 424
Db 458 FNELRKRYKVTENILSITQOGWDORIGELAGITRNGDRIQSGKAYVDYLLKGEELAKHSDK 517
QY 425 LNLNKLQAEKVIAITQOQWMDNIGDLAGISRLGEKVLGKAYVDVAFEEGKHI-K-ADK 482
Db 518 FTKQLDLPKINIDLSGI-KGSTT-LTFLNPLLTAGKERKTQSGKYEFITELKVKGRT 575
QY 483 LV-Q-LDSANGIIDVNSGKAKTQHILFPTLLTPGTHERVQTGKYEYITKLNN-RV 539
Db 576 D-WKVGVPSNGVYDFSNLIQH-AVTRDN--KVL---EARLIANLGAKKDDYVFGSGST 628
QY 540 DSWKITDGAASS-TFDLTNYVQRIEILDNAGNVTKTETKIIAKLGEEDDNVFGSGTT 598
Db 629 IVNAGDGYVDVYSKGRGTALTIDGRNATKAGQYKVERDLSGTQVLQETVSKQETKRKV 688
QY 599 EIDGEGGYDRVHYSNGNYGALTIDATKETEQSGYTVNRFVETGKALHEVTHHTALVGNR 658
Db 689 TDLLEYRNYKLDYTYTNKGFKAHDELNSVEITIGTLRDKFYGSKFNDFVFGHGDGDDLIY 748
QY 659 EKEIYRHSN-NQHHA--GYITKDTLKAVEIIGTSHNDIFPKSFENDAFNGDGVDTID 715
Db 749 GYDGDRLRYGNGNDIEHGGGNGKLYGGAGNDRLFGYGN-NYLD-GGEGDDHLEGNG 806
QY 716 GNDGNDRLFGGKGDILDGGNGDDFIDGKGNLHGGKDDIFVHRKGGDNDIITSDSG 775
Db 807 SDILRGGSGNDK-L-FGNQGGDLL 828
QY 776 NDKLSFSDSNLKDUTTFEKVKHNLV 799
RESULT 12
ENTRY      S34238 #type fragment
TITLE      leukotoxin A - Pasteurella haemolytica (fragment)
ALTERNATE_NAMES ltxA protein
ORGANISM    #formal_name Pasteurella haemolytica
DATE        06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
               13-Mar-1997
ACCESSIONS  S34238; S34236
REFERENCE   S34235
#authors    Lalinson, A.F.; Altschison, K.D.; Donachie, W.
#submission submitted to the EMBL Data Library, June 1993
#description DNA sequence of the carboxy terminal end of leukotoxin A from
               the T4 serotype of Pasteurella haemolytica; DNA sequence of
               the carboxy terminal end of leukotoxin A from the T15
               serotype of Pasteurella haemolytica.
#accession  S34238
#status     preliminary
#molecule_type DNA
#residues   1-208 ##label LA1
#cross-references EMBL:222885; PID:g311831
#experimental_source serotype T4

```

```
#accession S34236
#status Preliminary
#molecule_type DNA
#residues 9-208 #label LA2
#cross-references EMBL:422886; PID:g311827
#experimental_source serotype T15

GENETICS
#gene lktA
#superfamily hemolysin A; hemolysin A homology
#calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
#tandem repeat
#length 208 #checksum 8349

Query Match 19.4%; Score 1208; DB 2; Length 208;
Best Local Similarity 82.2%; Pred. No. 1.43e-141;
Matches 171; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Db 1 GNDRLFGKGGDDIDGGNGDDFDGKGNDLLHGGKGGDDIFVHRGGDNDSDITESEGNK 60
QY 719 GNDRLFGKGGDDIDGGNGDDFDGKGNDLLHGGKGGDDIFVHRGGDNDITDSGNK 778

Db 61 LSFSDSNLKDITFEKVNHLVITNTKOEKVTIQNWFREAEFAKTRINYYATRDDKIEEII 120
QY 779 LSFSDSNLKDITFEKVNHLVITNTKOEKVTIQNWFREAEFAKTRINYYATRDDKIEEII 838

Db 121 GNGERITSKQVDELEIKGKIDKSDLSQVVDNTQLLYKSDASNSLDKLSSASFTS 180
QY 839 GNGERITSKQVDDLIKANGKITQDELKSVYDNYELLKHSKNVTNSLDKLSSVSFTS 898

Db 181 SNDNRNLASPTSMLDPSLSISQIFARAA 208
QY 899 SNDNRNLVAPTSMLDQSLSSLOFARGS 926

RESULT 13
ENTRY #type complete
TITLE cyclolysin - Bordetella pertussis
ALTERNATE_NAMES adenylate cyclase precursor; calmodulin-sensitive adenylate
cyclase-hemolysin bifunctional protein
CONTAINS adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive;
hemolysin
ORGANISM #formal_name Bordetella pertussis
DATE 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
05-Sep-1997
ACCESSION S00893; S14100; S02389
REFERENCE S00893
#authors Glaser, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.;
Danchin, A.
#journal Mol. Microbiol. (1988) 2:19-30
#title The calmodulin-sensitive adenylate cyclase of Bordetella
pertussis: cloning and expression in Escherichia coli.
#cross-references MUID:88216178
#accession S00893
#molecule_type DNA
#residues 1-1706 #label GLA
#cross-references EMBL:Y00545; NID:g396665; PID:g396666
REFERENCE S02386
#authors Glaser, P.; Sakamoto, H.; Bellaloui, J.; Ullmann, A.; Danchin,
A.
#journal EMBO J. (1988) 7:3997-4004
#title Secretion of cyclolysin, the calmodulin-sensitive adenylate
cyclase-haemolysin bifunctional protein of Bordetella
pertussis.
#cross-references MUID:89091151
#contents annotation: identification of adenylate cyclase--hemolysin
bifunctional protein
REFERENCE S14100
#authors Munier, H.; Gilles, A.M.; Glaser, P.; Krin, E.; Danchin, A.;
Sarfati, R.; Barzu, O.
#journal Eur. J. Biochem. (1991) 196:469-474
#title Isolation and characterization of catalytic and
calmodulin-binding domains of Bordetella pertussis
adenylate cyclase.
```

```
#cross-references MUID:91177021
#accession S14100
#molecule_type protein
#residues 1-78, 'M', '80', 'M', '82-97', 'M', '99-139', 'M', '141-178', 'M', '180-399'
#label MUN

REFERENCE A55167
#authors Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Hewlett,
E.L.
#journal Science (1994) 266:433-435
#title Internal lysine palmitoylation in adenylate cyclase toxin
from Bordetella pertussis.
#contents annotation: lysine palmitoylation
B. pertussis, the etiological agent of whooping cough, disrupts
mammalian cell function by causing elevation of cAMP
concentration. The enhancement of cAMP synthesis is partly due to
activation by host cell calmodulin of the adenylate cyclase
activity of bacterial cyclolysin, which is synthesized as a large
bifunctional precursor also carrying hemolytic activities.
Adenylate cyclase activity is activated upon binding of calmodulin
in the vicinity of Trp-242.

GENETICS
#gene cyaA; cya
#superfamily cyclolysin; calmodulin-sensitive adenylate
cyclase catalytic domain homology; hemolysin A homology
#calcium binding; calmodulin binding; cAMP biosynthesis;
carbon-oxygen lyase; hemolysis; lipoprotein;
phosphorus-oxygen lyase; tandem repeat; toxin; whooping
cough

FEATURE
15-328 #domain calmodulin-sensitive adenylate cyclase catalytic
domain homology #label ADE\
25-35 #region calmodulin binding #status predicted\
59-66 #region nucleotide binding #status predicted\
544-1085 #domain hemolysin A homology #label HEM\
1033-1041,
1042-1050,
1174-1182,
1289-1297,
1298-1308,
1316-1324,
1430-1438,
1556-1564
993 #region repeats\
#binding_site palmitate (Lys) (covalent) #status
experimental

SUMMARY #length 1706 #molecular-weight 177506 #checksum 6461
Query Match 14.4%; Score 896; DB 1; Length 1706;
Best Local Similarity 32.0%; Pred. No. 2.76e-98;
Matches 191; Conservative 165; Mismatches 212; Indels 29; Gaps 26;

Db 530 GGFVGAGMALGGIAAAVAGMSLTD-DAPAGOKAAGAEIALQLTGGTVELASSIAL 588
QY 197 GGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAFELANQVGNITKAVSSV-I 255

Db 589 ALAARGVTSLGVAGASAGAAALAAALSPMEIYGLVQOSHADQLDKLAOESSATGY 648
QY 256 -LAQ-R-VAAGLSSTGPVAAITASTVSLAISPLAFAGTADKFNHAKSLSEYAEKKILGY 312

Db 649 EGDALLAOLYRDKTAEGAVAGVSAVLSTVGAASVIAAAASVVGAPVAVVTSLTGALNG 708
QY 313 DGDNLAEYQRTGTIDASTVTAINTALAAIAGVSAAGSVIAPIALLVSGITGVIST 372

Db 709 ILRGVQQPIIEKLANDYARKI-D-ELGGP-QAYFEKNLQARHEQLANSGLRKLADLQA 765
QY 373 ILQYSQAMFEHVANKINKIVEKNNHKNYFENGVDARY--LANLDNNMKFLNLNK 430

Db 766 GWNASVITGVOTETSKSALEALATIGNADNLKSVDFVDFVQGERVAGQPVV-LDVAA 824
QY 431 ELQAEVIAITQQQNDNIGDLGIRLGEKVLSCAKYVDVAFEECKHIKADKLVDLSAN 490

Db 825 GGDIDIASR-KGERPALTTITPLAAPGEORRTKTKGSEFTTVEIVGKQDWRIRDGAA 883
QY 491 GIIDVSNSGKAKTQHLFTPLLTGTEHREVRVOTGKYEITKLNI-NRVDWSKITDGAA 549
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Db 884 DTTIDLAKVVSQ-L-VD-AN-G-VLK-HSIKLDVIGGDDVVVLANSRIHYDGGAGTNTV 938
QY 550 SSTFDLTNNVQIGIELDNAGNTKTKETKIIAKLGGEDDNNVFVSGTTEIDGEGYDRV 609
Db 939 SYAALGRQDSITVSA--DGER--FNVRKOLNANVYREGVATQTAAYGKRTENVQYRHVE 994
QY 610 HYSR-GNYGALITDATKETEGGSTVYVNRFTGKALHEVSTHTALVGNREEKIEYRHSN 668
Db 994 LARVGQVVEVDTLHVQHIIIGGAGNDSITGNAHNFLLAGSGDRLDGGAGNDTLVGGEG 1054
QY 669 NOHHAGYYTKDTLKAVEEIICTSHNDIFKSKFNDAFNGGVDITDGNCGNDRLFGGKG 728
Db 1055 QNTVIGGAGDDVFLQDLGVWSNQLDGGAGVDTVKYNNVHQPSEERLERMGDTGIHADL 1111
QY 729 DDILDGGNGDD-FIDG-GKGNLHLHGKG-DDI-F-VHRKGDGN-DIITDSGNDKL 779

RESULT 14          S51672      #type complete
ENTRY      adenylate cyclase hemolysin - Bordetella bronchiseptica
TITLE      #formal_name Bordetella bronchiseptica
ORGANISM   07-May-1995 #sequence_revision 01-Sep-1995 #text_change
DATE       23-May-1997
ACCESSIONS S51672
REFERENCE   S51672
#authors   Betson, F.; Sismeiro, O.; Danchin, A.; Guiso, N.
#submission submitted to the EMBL Data Library, September 1994
#description The adenylate cyclase-hemolysin gene from Bordetella
              bronchiseptica.
#accession S51672
#status    Preliminary
#molecule_type DNA
#residues  1-1705 #label BET
#cross-references EMBL:237112
CLASSIFICATION #superfamily cyclolysin; calmodulin-sensitive adenylate
                cyclase catalytic domain homology; hemolysin A homology
KEYWORDS     tandem repeat
FEATURE      15-328
543-1084
SUMMARY      #length 1705 #molecular-weight 177313 #checksum 3352
              #domain calmodulin-sensitive adenylate cyclase catalytic
              domain homology #label ADE\
              #domain hemolysin A homology #label HEM
              #length 1705 #molecular-weight 177313 #checksum 3352
Query Match 14.3%; Score 887; DB 2; Length 1705;
Best Local Similarity 31.8%; Pred. No. 4.77e-97;
Matches 190; Conservative 165; Mismatches 212; Indels 30; Gaps 27;

Db 530 GGFVAGAGMALGGI-GAVGAGSLTD-DAPAGOKAAGAEIALQLTGGTVELASSIAL 587
QY 197 GGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKYGAGFELANQVGNITKAVSSY-I 255
Db 588 ALAARGVTSGLQVAGASAGAAALAAALSPMETYGLVQOSHVAQDLQKLAQESSAYGY 647
QY 256 -LAQ-R-VAAGLSSTGPVAAIISTVSLAISPLAFAGIADFNHAKSLESYAEERFKLGY 312
Db 648 EGDALLAOLYRDKTAEGAVAGSVAIVTGAASVIAAASVAGPVAIVTSLITGALNG 707
QY 313 DGDNLAEYQRTGTIDASVTAINTALAAIAGVSAAGSVIASPIALLVSGITGVIST 372
Db 708 ILRGVQQPILIEKLANDYARKI-D-ELGGP-QAYPEKNLQARHEOLANSDDLRLMLADLQA 764
QY 373 ILQYSKQAMFEHVANKIHNKIVWEKNNHGNKYPENGVDARY--LANIQDNKFFLLNLK 430
Db 765 GWNASSVIGVQTTEISKSALEALATIGNADNLKSADEVFVDFRFIGERVAGQPVV-LDVAA 823
QY 431 ELQAEVIAITQQQWNNIGDLGISRLGKVLSCAYDAFEEGKHKADKLVLQDSAN 490
Db 824 GGIDIASR-KGERPALFITPLAPGEEQRRTTKGSEFTTFVEIVGKQDWRIRGAA 882
QY 491 GIIDVNSGKAKTQHILFRTPLLTPGTEHRRERVOTGKYEYITTKLNI-NRVDSWKITDGA 549
Db 883 DTTIDLAKVVSQ-L-VD-AN-G-VLK-HSIKLEIVIGGDDVVVLANSRIHYDGGAGTNTV 937
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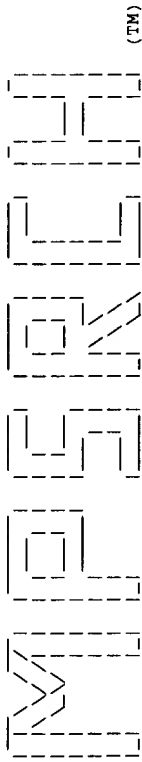
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QY 550 SSTFDLTNNVQIGIELDNAGNTKTKETKIIAKLGGEDDNNVFVSGTTEIDGEGYDRV 609
Db 938 SYAALGRQDSITVSA--DGER--FNVRKOLNANVYREGVATQTAAYGKRTENVQYRHVE 993
QY 610 HYSR-GNYGALITDATKETEGGSTVYVNRFTGKALHEVSTHTALVGNREEKIEYRHSN 668
Db 994 LARVGQVVEVDTLHVQHIIIGGAGNDSITGNAHNFLLAGSGDRLDGGAGNDTLVGGEG 1053
QY 669 NOHHAGYYTKDTLKAVEEIICTSHNDIFKSKFNDAFNGGVDITDGNCGNDRLFGGKG 728
Db 1054 HNTVVGAGDDVFLQDLGVWSNQLDGGAGVDTVKYNNVHQPSEERLERMGDTGIHADL 1110
QY 729 DDILDGGNGDD-FIDG-GKGNLHLHGKG-DDI-F-VHRKGDGN-DIITDSGNDKL 779

RESULT 15          S35027      #type complete
ENTRY      cytotoxin RTX homolog frpC - Neisseria meningitidis
TITLE      #formal_name Neisseria meningitidis
ORGANISM   03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
DATE       09-Sep-1997
ACCESSIONS S35027
REFERENCE   S35026
#authors   Thompson, S.A.; Wang, L.L.; Sparling, P.F.
#journal    Mol. Microbiol. (1993) 9:85-96
#title      Cloning and nucleotide sequence of frpC, a second gene from
              Neisseria meningitidis encoding a protein similar to RTX
              cytotoxins.
#accession S35027
#molecule_type DNA
#residues  1-1829 #label THO
#cross-references GB:L06299; NID:g293961; PID:g293963
GENETICS
#gene      frpC
SUMMARY      #length 1829 #molecular-weight 197622 #checksum 8960
              Query Match 4.6%; Score 286; DB 2; Length 1829;
              Best Local Similarity 31.8%; Pred. No. 7.59e-18;
              Matches 70; Conservative 60; Mismatches 71; Indels 19; Gaps 18;

Db 952 AKDDSGGVTVQSYFONDGSGAYRIDEIHFONGKVL-DVATV-KELVQOSTDSDRLYAYQ 1009
QY 612 SRNYGALTIDATKETE-QGSYTVNRF-VETGKALHEVSTHTALVGNREEKIE--YR-H 666
Db 1010 SGNTLNGGL-GDDYLYGAGDGDLLNGDAGNDSIYSGNG-NDTLNGGEGNDALXYNGNDA 1067
QY 667 SNQHHAGYYTKDTL-KA-VEEII-G-TSHNDFKSGKFNDAFNGGVDITDGNCGNDR 722
Db 1068 LNGGEGNDHLNGEDGNDTLIGGAGNDYLEGSGSDIYVFGKFGODTVYNYDYATGRKDI 1127
QY 723 LFGGKGDDILDGGNGDDFIDGKGNDLLHGKGDIFVHRKGDGNDII-T-D-SDG-NDK 778
Db 1128 IRTFDGITADMLAFTREGNHLIIKAKDGSQGVTVQSYFQN 1167
QY 779 LSFSDSNLKD-LIFERVKVHNLVI-TNSKKEKVTONWFE 816

Search completed: Wed Dec 9 19:23:12 1998
Job time : 176 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Dec 9 19:23:29 1998; MasPar time 25.63 Seconds  
980.165 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-455-970-12  
Description: (1-936) from US08455970.pep  
Perfect Score: 5217  
Sequence: 1 MATVIDLSPFKTGAKKILY.....LSSLOFARGSOHWSYGLRPG 936

Scoring table: PAM 150  
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot35  
1:swissprot

Statistics: Mean 57.021; Variance 139.964; scale 0.407

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	6049	97.3	953	1	HLAL_PASHA	0.00e+00
2	5743	92.4	953	1	HLAB_PASHA	0.00e+00
3	5560	89.4	953	1	HLA3_PASHA	0.00e+00
4	5510	88.6	955	1	HLAA_PASHA	0.00e+00
5	5020	80.7	947	1	HLIA_PASBP	0.00e+00
6	4354	68.4	956	1	RT2A_ACTPL	0.00e+00
7	4205	67.6	956	1	HLYA_ACTSU	0.00e+00
8	2616	42.1	1052	1	RT32_ACTPL	0.00e+00
9	2566	41.3	1049	1	RT31_ACTPL	0.00e+00
10	2398	38.6	1023	1	HLV1_ECOLI	0.00e+00
11	2384	38.3	1024	1	HLV1_ECOLI	0.00e+00
12	2244	36.1	1023	1	RT12_ACTPL	0.00e+00
13	2236	36.0	1023	1	RT11_ACTPL	0.00e+00
14	2167	34.9	1050	1	HLVA_ACTAC	0.00e+00
15	896	14.4	1706	1	CYAA_BORPE	9.23e-119
16	887	14.3	1705	1	CYAA_BORPE	2.89e-117
17	286	4.6	1829	1	FRPC_NEIME	8.54e-22
18	265	4.3	1115	1	FRPA_NEIME	8.30e-19
19	202	3.2	491	1	ZAPA_PROMI	3.02e-10
20	187	3.0	476	1	LIPB_PSEFL	2.52e-08
21	173	2.8	284	1	NODO_RHLV	1.38e-06
22	165	2.7	475	1	PRTG_ERWCH	1.29e-05
23	166	2.7	479	1	PRTC_ERWCH	9.75e-06

24	170	2.7	481	1	PRTB_ERWCH	SECRETED PROTEASE B PR	3.21e-06
25	164	2.6	472	1	PRTA_ERWCH	SECRETED PROTEASE A PR	1.69e-05
26	162	2.6	478	1	PRTX_ERWCH	SECRETED PROTEASE C PR	2.93e-05
27	159	2.6	3591	1	PHAB_BORPE	FILAMENTOUS HEMAGGLUTI	6.62e-05
28	152	2.4	449	1	LIPA_PSEFL	LIPASE PRECURSOR (EC 3	4.31e-04
29	150	2.4	479	1	APRA_PSEAE	ALKALINE METALLOPROTEI	7.30e-04
30	147	2.4	487	1	PRZN_SERMA	SERRALYSIN PRECURSOR (	1.60e-03
31	137	2.2	1574	1	MYS2_YEAST	MYOSIN-2 ISOFORM.	2.04e-02
32	133	2.1	486	1	PRZN_SERSP	SERRALYSIN PRECURSOR (	5.50e-02
33	133	2.1	550	1	KUCR_RAT	KUPFFER CELL RECEPTOR	5.50e-02
34	132	2.1	749	1	MAD1_YEAST	SPINDLE ASSEMBLY CHECK	7.02e-02
35	133	2.1	1959	1	MYSN_CHICK	MYOSIN HEAVY CHAIN, (H	5.50e-02
36	133	2.1	2035	1	HFCL_HUMAN	HOST CELL FACTOR C1 (H	5.50e-02
37	131	2.1	2249	1	190K_RICRI	190 KD ANTIGEN PRECURS	8.95e-02
38	122	2.0	390	1	FLAA_BORBR	FLAGELLIN.	7.56e-01
39	122	2.0	682	1	PILA_PSEAE	PILJ PROTEIN.	7.56e-01
40	123	2.0	1025	1	SLAP_CAUCR	S-LAYER PROTEIN (PARAC	5.99e-01
41	124	2.0	2541	1	TALI_MOUSE	TALIN.	4.75e-01
42	121	1.9	344	1	Y09A_MYCTU	HYPOTHETICAL 35.1 KD P	9.51e-01
43	121	1.9	409	1	Y291_MEIJA	PROBABLE SIGNAL RECOGN	9.51e-01
44	121	1.9	754	1	KATC_ARATH	KINESIN-LIKE PROTEIN C	9.51e-01
45	121	1.9	2491	1	TALA_DICDI	FILPODIN (TALIN HOMOL	9.51e-01

ALIGNMENTS

RESULT 1	HLAL_PASHA	STANDARD;	PRT;	953 AA.
AC	PI6535;			
DT	01-AUG-1990 (REL. 15, CREATED)			
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	LEUKOTOXIN FROM SEROTYPE A1.			
GN	LKTA.			
OS	PASTURELLA HAEMOLYTICA.			
OC	PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	PASTURELLACEAE.			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=SEROTYPE A1;			
RX	MEDLINE: 87306837.			
RA	LO R.Y.C.; STRATHDEE C.A.; SHEWEN P.E.;			
RL	INFECT. IMMUN. 55:1987-1996(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PHL101 / SEROTYPE A1;			
RX	MEDLINE: -89210283.			
RA	HIGHLANDER S.K.; CHIDAMBARAM M., ENGLER M.J., WEINSTOCK G.M.;			
RL	DNA 8:15-28(1989).			
RN	[3]			
RP	SEQUENCE OF 884-953 FROM N.A.			
RC	STRAIN=PHL101 / SEROTYPE A1;			
RX	MEDLINE: 90236888.			
RA	HIGHLANDER S.K.; ENGLER M.J., WEINSTOCK G.M.;			
RL	J. BACTERIOL. 172:2343-2350(1990).			
CC	-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD			
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY			
CC	DEFINED.			
CC	-1- SUBCELLULAR LOCATION: SECRETED.			
CC	-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING			
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC			
CC	ACTIVITY.			
CC	-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE			
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).			
CC	-1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE			
CC	STRUCTURAL TOXIN).			
DR	EMBL: M20730; G150494; -			
DR	EMBL: M24197; G150513; -			
DR	PIR: S29516; S29516.			
DR	HSSP: P02392; ICTF.			
DR	PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.			
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;			
KW	TRANSMEMBRANE.			



```
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 366 390 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH (BY SIMILARITY).
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
FT CONFLICT 409 414 FERHAN -> LSTLOI (IN REF. 2).
FT CONFLICT 742 742 D -> Y (IN REF. 2).
SQ SEQUENCE 953 AA; 101996 MW; 40FB25EB CRC32;

Query Match
Best Local Similarity 97.3%; Score 6049; DB 1; Length 953;
Matches 914; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 38 KTGAKKIILYIPONYQYDTEQGNGLQDLVKAAREELGIEVQREERNNTAQTSLGTIQT 97
QY 11 KTGAKKIILYIPONYQYDTEQGNGLQDLVKAAREELGIEVQREERNNTAQTSLGTIQT 70

Db 98 IGLTERGIVLSAPQIDKLLQKTAGAGALSAESIVQNAKAKTVLSGIQSLGSLAGMD 157
QY 71 IGLTERGIVLSAPQIDKLLQKTAGAGALSAESIVQNAKAKTVLSGIQSLGSLAGMD 130

Db 158 LDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGKLNKIGLGTIG 217
QY 131 LDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGKLNKIGLGTIG 190

Db 218 DKLKNGIGGLDAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELANOVGNITKA 277
QY 191 DKLKNGIGGLDAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELANOVGNITKA 250

Db 278 VSSYILAQRVAAGLSTGPVAALIASTVLSLAISPLAFAGIADKFNAKLSVAERFKL 337
QY 251 VSSYILAQRVAAGLSTGPVAALIASTVLSLAISPLAFAGIADKFNAKLSVAERFKL 310

Db 338 GYDGDNLLEYRGTTIDASVTAINALAAIAGGVSAAAAGSVIASPIALLVSGTIGYI 397
QY 311 GYDGDNLLEYRGTTIDASVTAINALAAIAGGVSAAAAGSVIASPIALLVSGTIGYI 370

Db 398 STILOYSKOAMFEHVANKTHNKIVKKNHNGKNYFENGVDARYLANLODNKKFLNLNK 457
QY 371 STILOYSKOAMFEHVANKTHNKIVKKNHNGKNYFENGVDARYLANLODNKKFLNLNK 430

Db 458 ELQAEVIAITQQQDNNDIGDLAGISRLGKVLGRAYVDVAFEGKHAKADKLVLQDLSAN 517
QY 431 ELQAEVIAITQQQDNNDIGDLAGISRLGKVLGRAYVDVAFEGKHAKADKLVLQDLSAN 490

Db 518 GIIDVNSGAKTQHILFRPLTPTGTEHRERVQTKYIYITKLINRVDSWKITDGAAS 577
QY 491 GIIDVNSGAKTQHILFRPLTPTGTEHRERVQTKYIYITKLINRVDSWKITDGAAS 550

Db 578 STFDLTNVVQRIEGLDNAGNVTKTKETKIIAKLGGDDNVFVSGTTEIDGEGYDRVH 637
QY 551 STFDLTNVVQRIEGLDNAGNVTKTKETKIIAKLGGDDNVFVSGTTEIDGEGYDRVH 610

Db 638 YSRGNYGALTIDATKTEQGSYTVNRFVETGKALHEVTSTHTALVNREKTEYRHSNQ 697
QY 611 YSRGNYGALTIDATKTEQGSYTVNRFVETGKALHEVTSTHTALVNREKTEYRHSNQ 670

Db 698 HHAGYTTKTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGQGVDTIDGNDNDRLFGGKGD 757
QY 671 HHAGYTTKTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGQGVDTIDGNDNDRLFGGKGD 730

Db 758 ILDGGNGDDFIDGKGNLHLHGKGGDDIFVHRKGDNDNIITSDGNDKLSFSDSNLKDIT 817
QY 731 ILDGGNGDDFIDGKGNLHLHGKGGDDIFVHRKGDNDNIITSDGNDKLSFSDSNLKDIT 790

Db 818 FEKVKNLVTNKKKVKVITQNWFRADFAKEVPNYKATKDEKIEIIGONGERITSKV 877
QY 791 FEKVKNLVTNKKKVKVITQNWFRADFAKEVPNYKATKDEKIEIIGONGERITSKV 850
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Db 878 DDLIAKNGKITQDELSKVVDNYELLKHKSNVTNSLDKLSSVSFTSSNDSNRNLVAPT 937
QY 851 DDLIAKNGKITQDELSKVVDNYELLKHKSNVTNSLDKLSSVSFTSSNDSNRNLVAPT 910

Db 938 SMLDOSLSLQFARAA 953
QY 911 SMLDOSLSLQFARGS 926

RESULT 2
ID HLAB PASHA STANDARD; PRT; 953 AA.
AC P55118;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN FROM SEROTYPE A11.
GN LKTA.
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE A11;
RX MEDLINE; 94041617.
RA BURROWS L.L., OLAH-WINFIELD E., LO R.Y.C.;
RL INFECT. IMMUN. 61:5001-5007(1993).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).
DR EMBL; U01215; G397992; -.
KW PROSITE; PS00330; HEMOLYSIN-CALCIUM; 4.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 230 250 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
SQ SEQUENCE 953 AA; 102206 MW; 321C9369 CRC32;
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Query Match
Best Local Similarity 92.4%; Score 5743; DB 1; Length 953;
Matches 856; Conservative 37; Mismatches 23; Indels 0; Gaps 0;

Db 38 KTGAKKIILYIPKDYQDTEKGNGLDLVKAAREELGIEVQREERNNTAQTSLGTIQT 97
QY 11 KTGAKKIILYIPQNTQYDTEQGNGLQDLVKAAREELGIEVQREERNNTAQTSLGTIQT 70

Db 98 IGLTERGIVLSAPQIDKLLQKTAGAGALSAESIVQNAKAKTVLSGIQSLGSLAGMD 157
QY 71 IGLTERGIVLSAPQIDKLLQKTAGAGALSAESIVQNAKAKTVLSGIQSLGSLAGMD 130

Db 158 LDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGKLNKIGLGTIG 217
QY 131 LDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGKLNKIGLGTIG 190

Db 218 DKLKGLSGFDKTSGLDGVVSGLLSGATAALVLADKNASTSRKVAGAGFELANOVGNITKA 277
QY 191 DKLKNGIGGLDAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELANOVGNITKA 250
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Db 278 VSSYLAORVAAGLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 337
QY 251 VSSYLAORVAAGLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 310
Db 338 GYDGNLLAEYQRTGTTIDRSVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 397
QY 311 GYDGNLLAEYQRTGTTIDRSVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 370
Db 398 STILOYSKOAMFEHVANKIHKNKIVWEKNHGNKNTFENGVDARYLANLODNMKFLNLNK 457
QY 371 STILOYSKOAMFEHVANKIHKNKIVWEKNHGNKNTFENGVDARYLANLODNMKFLNLNK 430
Db 458 ELQAEVTAITQQQWNNIGDLGSRGKVLGSKAYVDAFEKGKHLKADKLVOLDSAN 517
QY 431 ELQAEVTAITQQQWNNIGDLGSRGKVLGSKAYVDAFEKGKHLKADKLVOLDSAN 490
Db 518 GIIDVSNKSKAKTQHLFRTPLTPTGTEHRRVQTKYEYITKLNINRVDSWKIIDGAAS 577
QY 491 GIIDVSNKSKAKTQHLFRTPLTPTGTEHRRVQTKYEYITKLNINRVDSWKIIDGAAS 550
Db 578 STFDLTNNVQRIEIDNAGNVTKTKETKIIVAKLGAGDDNVFVSGTTEIDGEGYDRVH 637
QY 551 STFDLTNNVQRIEIDNAGNVTKTKETKIIVAKLGAGDDNVFVSGTTEIDGEGYDRVH 610
Db 638 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 697
QY 611 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 670
Db 698 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNNDNRLFPGKDD 757
QY 671 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNNDNRLFPGKDD 730
Db 758 IIDGGNGDDFIDGKGNLHGGKDDIFVHRQGDNDIITDSGNDKLSFSDSNLKDIT 817
QY 731 IIDGGNGDDFIDGKGNLHGGKDDIFVHRQGDNDIITDSGNDKLSFSDSNLKDIT 790
Db 818 FEKVHNLVITNSREKVTIQDFREADFAKEVRYNKKATKDEKIEIIGQGERITSQV 877
QY 791 FEKVHNLVITNSREKVTIQDFREADFAKEVRYNKKATKDEKIEIIGQGERITSQV 850
Db 878 DDLIAGKNGKITQDELKSKVDNYELLKSKNVTNSLDKLISASAFSTNSDRNVLVAPT 937
QY 851 DDLIAGKNGKITQDELKSKVDNYELLKSKNVTNSLDKLISASAFSTNSDRNVLVAPT 910
Db 938 SMDQSLSSLOFARAA 953
QY 911 SMDQSLSSLOFARGS 926

RESULT 3
ID HLA3-PASHA STANDARD: PRT: 953 AA.
AC P55116;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN FROM SEROTYPE T3.
GN LKTA.
OS PASTEURELLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE T3;
RX MEDLINE; 94041617.
RA BURROWS L.L., LO R.Y., OLAH-WINFIELD E.;
RL INFECT. IMMUN. 61:5001-5007(1993).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC -!- CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC

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CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL; U01216; G397995; -.
DR PROSITE; PS00330; HEMOLYSIN-CALCIUM; 2.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
SQ SEQUENCE 953 AA; 101948 MW; FFED778E CRC32;

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Query Match 89.4%; Score 5560; DB 1; Length 953;
Best Local Similarity 89.2%; Pred. No. 0.00e+00;
Matches 817; Conservative 55; Mismatches 44; Indels 0; Gaps 0;

Db 38 KNGVKKIILYIPKDYKSGSGNGLDLVKAAEELGIEVQKEEGNDIAKAQTSIGTQNV 97
QY 11 KTGAKKIILYIPQNYQYDEQNGLDLVKAAEELGIEVQKEEGNDIAKAQTSIGTQ 70
Db 98 LGLTERGVLSAPOLDKLLQNKVQALGSSSEIAQNFQAKTQVLSGVQSLGSLVLAGMD 157
QY 71 LGLTERGVLSAPQIDKLLQNKVQALGSSSEIAQNFQAKTQVLSGVQSLGSLVLAGMD 130
Db 158 LDEALQNESDQTLAKAGLELTNSLIENANSVOTLDAFSEQISOFGSKLQNVKGLGALG 217
QY 131 LDEALQNNQNHAKAGLELTNSLIENANSVOTLDAFSEQISOFGSKLQNVKGLGALG 190
Db 218 DKLKNIGGLDAGLGLHVISGLLSGATAALVLADKADSTAKKVGAGFELANOVGNITKA 277
QY 191 DKLKNIGGLDAGLGLHVISGLLSGATAALVLADKADSTAKKVGAGFELANOVGNITKA 250
Db 278 VSSYLAORVAARLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 337
QY 251 VSSYLAORVAARLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 310
Db 338 GYEGDLSLAIEYQHGTTIDASVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 397
QY 311 GYEGDLSLAIEYQHGTTIDASVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 370
Db 398 STILOYSKOAMFEHVANKIHKNKIVWEKNHGNKNTFENGVDARYLANLODNMKFLNLNK 457
QY 371 STILOYSKOAMFEHVANKIHKNKIVWEKNHGNKNTFENGVDARYLANLODNMKFLNLNK 430
Db 458 ELQAEVTAITQQQWNNIGDLGSRGKVLGSKAYVDAFEKGKHLKADKLVOLDSAN 517
QY 431 ELQAEVTAITQQQWNNIGDLGSRGKVLGSKAYVDAFEKGKHLKADKLVOLDSAN 490
Db 518 GIIDVSNKSKAKTQHLFRTPLTPTGTEHRRVQTKYEYITKLNINRVDSWKIIDGAAS 577
QY 491 GIIDVSNKSKAKTQHLFRTPLTPTGTEHRRVQTKYEYITKLNINRVDSWKIIDGAAS 550
Db 578 STFDLTNNVQRIEIDNAGNVTKTKETKIIVAKLGAGDDNVFVSGTTEIDGEGYDRVH 637
QY 551 STFDLTNNVQRIEIDNAGNVTKTKETKIIVAKLGAGDDNVFVSGTTEIDGEGYDRVH 610
Db 638 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 697
QY 611 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 670
Db 698 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNNDNRLFPGKDD 757
QY 671 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNNDNRLFPGKDD 730

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Db 758 IIDGGNGDDFIDGGKGNHLLHGGKGVDFVHRQDGNDSITSEGNKLSFSDSNLKDLT 817
Qy 731 ILDDGGNGDDFIDGGKGNLHLLHGGKGVDFVHRKGDGDDIITDSGNDKLSFSDSNLKDLT 790
Db 818 FEKVNHLVITNTKOEKVITQNWFEAEFAKTQNYVATRDCKIEEIIQNGERITSKVQV 877
Qy 791 FEKVKNHLVITNSKKEKVTIQNWFEADFAKEVPNYKATDEKIEEIIQNGERITSKVQV 850
Db 878 DDLIAKNGKIAQSELTKVVDNYQLLYKSRDASNSLDKLISSAFAFTSSNDSRNVLASPT 937
Qy 851 DDLIAKNGKITODELKVVDNYELLKHKNVTNSLDKLISSAFAFTSSNDSRNVLASPT 910
Db 938 SMLDPSLSSIQFARAA 953
Qy 911 SMLDQSLSSIQFARGS 926

RESULT 4
ID HLAA_PASHA STANDARD; PRT; 955 AA.
AC P55117;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN FROM SEROTYPE T10.
GN LKTA.
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RC STRAIN-SEROTYPE T10;
RA LAINSON A.F., MURRAY J., DAVIES R.C., DONACHIE W.;
RL MICROBIOLOGY 142:2499-2507(1996).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL; Z26247; G400425; -
DR PROSITE; PS00330; HEMOLYSIN-CALCIUM; 4.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 299 319 POTENTIAL.
FT TRANSMEM 361 381 POTENTIAL.
FT TRANSMEM 383 403 POTENTIAL.
FT DOMAIN 736 786 6 X REPEATS, GLY-RICH.
FT REPEAT 736 741 1.
FT REPEAT 745 750 2.
FT REPEAT 754 759 3.
FT REPEAT 763 768 4.
FT REPEAT 772 777 5.
FT REPEAT 781 786 6.
SQ SEQUENCE 955 AA; 102187 MW; AA440A0A CRC32;

Query Match 88.6%; Score 5510; DB 1; Length 955;
Best Local similarity 88.4%; Pred. No. 0.00e+00;
Matches 810; Conservative 60; Mismatches 46; Indels 0; Gaps 0;

Db 40 KNGAKKIILYIPKDYKDYSGNGSLQDLVKAABEELGIEVQKEEGNDIAKAQTSIGTIQNV 99
Qy 11 KTGAKKIILYIPQYQYDTEOGNGLQDLVKAABEELGIEVQREERNNTAQTSLGTIQT 70
Db 100 LGLTERGIVLSAPOLDKLLQNKVQALGSSESTAQNFSAQKTVLSGVQNSRRTVLGMD 159
Qy 71 IGLTERGIVLSAPOLDKLLQNKVQALGSSESTAQNFSAQKTVLSGVQNSRRTVLGMD 130
Db 160 LDEALQNESDQTLAKAGLELTNSLIENIANSVQTLDAFSQISQFGSKLQNVKGLGALG 219

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Qy 131 LDEALQNNNQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKLQNKGLTGL 190
Db 220 DKKNIGGLDKAGLGLDYKSRLLSGATAALVLADKDAKSTAKKYAGAGFELANQVVGNTKA 279
Qy 191 DKKNIGGLDKAGLGLDVISGLLSGATAALVLADKDAKSTAKKYAGAGFELANQVVGNTKA 250
Db 280 VSSYILAQRVAAGLSSSTGPVAALIASTVAIVASPLSPAGIADKFRKAKSLNVAERFKKL 339
Qy 251 VSSYILAQRVAAGLSSSTGPVAALIASTVSLAISPLAFAGIADKFRKAKSLNVAERFKKL 310
Db 340 GYEGDSLLAEVQHGCTGTDASVTAINALAAIAGGVSAAGVVAASPIALLVSGITGVI 399
Qy 311 GYDGNLLAEYQRTGTIDASVTAINALAAIAGGVSAAGVVAASPIALLVSGITGVI 370
Db 400 STILQYSKQAMFEHVANKIHNKIVVEKNGKNYFENGVDARYLANLQNMKFLNLNK 459
Qy 371 STILQYSKQAMFEHVANKIHNKIVVEKNGKNYFENGVDARYLANLQNMKFLNLNK 430
Db 460 ELQAEVIAITQOQWDSNIGDLAGISRLGEKVLSGKAYVDAFEEGQHLKADKLVQLDSAK 519
Qy 431 ELQAEVIAITQOQWDSNIGDLAGISRLGEKVLSGKAYVDAFEEGQHLKADKLVQLDSAN 490
Db 520 GIIDVTNTGEAKTQHILFRTPLTPGTEKREYVITKLHINRVDSQIKDCAAS 579
Qy 491 GIIDVNSGAKTQHILFRTPLTPGTEKREYVITKLHINRVDSQIKDCAAS 550
Db 580 STFDLTNVVQIRIGVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDGGEGYDRVH 639
Qy 551 STFDLTNVVQIRIGVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDGGEGYDRVH 610
Db 640 YSRNGYALIDATKETEQQSYTVNRFVSGKALHEGTSTHTALVGNREKIEYRHNNQ 699
Qy 611 YSRNGYALIDATKETEQQSYTVNRFVSGKALHEGTSTHTALVGNREKIEYRHNNQ 670
Db 700 HHAGYITKDTLKAEEIIGTSHNDIPKGSKFNDAGNGDGVDTIDGNDGNDRLFGGKGD 759
Qy 671 HHAGYITKDTLKAEEIIGTSHNDIPKGSKFNDAGNGDGVDTIDGNDGNDRLFGGKGD 730
Db 760 IIDGGNGDDFIDGGKGNLHLLHGGKGVDFVHRQDGNDSITSEGNKLSFSDSNLKDLT 819
Qy 731 ILDDGGNGDDFIDGGKGNLHLLHGGKGVDFVHRKGDGDDIITDSGNDKLSFSDSNLKDLT 790
Db 820 FEKVNHLVITNTKOEKVITQNWFEAEFAKTQNYVATRDCKIEEIIQNGERITSKVQV 879
Qy 791 FEKVKNHLVITNSKKEKVTIQNWFEADFAKEVPNYKATDEKIEEIIQNGERITSKVQV 850
Db 880 DELEKNGKIAQSELTKVVDNYQLLYKSRDASNSLDKLISSAFAFTSSNDSRNVLASPT 939
Qy 851 DDLIAKNGKITODELKVVDNYELLKHKNVTNSLDKLISSAFAFTSSNDSRNVLASPT 910
Db 940 SMLDPSLSSIQFARAA 955
Qy 911 SMLDQSLSSIQFARGS 926

RESULT 5
ID HLYA_PASSP STANDARD; PRT; 947 AA.
AC P55123;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN.
GN LKTA.
OS PASTEURILLA HAEMOLYTICA-LIKE SP. (STRAIN 5943B).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE; 9329320.
RA CHANG Y.-F., MA D.-P., SHI J., CHENGAPPA M.M.;
RL INFECT. IMMUN. 61:2089-2095(1993).
CC -!- FUNCTION: VIRULENCE FACTOR WHICH IS CYTOTOXIC FOR LEUKOCYTES BUT

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IS NOT HEMOLYTIC.  
 -!- SUBCELLULAR LOCATION: SECRETED.  
 -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING  
 CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC  
 ACTIVITY.  
 -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE  
 INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).  
 -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE  
 STRUCTURAL TOXIN).  
 EMBL: L12148; G457618; ...  
 DR PROSITE; PS00330; HEMOLYSIN\_CALCIUM; 4.  
 KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;  
 TRANSMEMBRANE.  
 FT TRANSMEM 154 170 POTENTIAL.  
 FT TRANSMEM 312 333 POTENTIAL.  
 FT TRANSMEM 393 414 POTENTIAL.  
 FT DOMAIN 625 780 7 X REPEATS, GLY-RICH.  
 FT REPEAT 625 630 1.  
 FT REPEAT 730 735 2.  
 FT REPEAT 739 744 3.  
 FT REPEAT 748 753 4.  
 FT REPEAT 757 762 5.  
 FT REPEAT 766 771 6.  
 FT REPEAT 775 780 7.  
 SQ SEQUENCE 947 AA; 101559 MW; 1D59473B CRC32;  
 Query Match 80.7%; Score 5020; DB 1; Length 947;  
 Best Local Similarity 78.6%; Pred. No. 0.00e+00;  
 Matches 720; Conservative 121; Mismatches 73; Indels 2; Gaps 2;  
 Db 34 KAGAKKILYIPKDYEGSRGQLDVLKAAEDLGIQVQERNGRTAONSLTQNI 93  
 QY 11 KTGAKKILYIPQNYQYDEGNGQLDVLKAAELGIEVQERNGRTAONSLTQI 70  
 Db 94 LGSERGVLSAPQDKLLQKYISKAPGSGSENVAKNLGNAGTLLSGIQSLGSMAGMD 153  
 QY 71 IGLTERGIVLSAPQDKLLQKTAKAGALGSAESIVQANAKAKTVLSGIQSLGSLVLAGMD 130  
 Db 154 LDEILKNGSELDLAKAGLELTNSLIENIANSVQTLDTFSEIQSLQTKLQNVKGLGTG 213  
 QY 131 LDEALQNNSHALAKAGLELTNSLIENIANSVKTLDFEGEIQSGFKLQNKIGLGTG 190  
 Db 214 DKLNFSGFKAGLGLVIGSLGATPAALVLADKNASTDRKVGAGFELANQVGNITKA 273  
 QY 191 DKLNIGLDRAGLGLVIGSLGATPAALVLADKNASTAKRVAGFELANQVGNITKA 250  
 Db 274 VSSYLAQVRAAGLSNTGSPVSAIATVASTVALAISPLAFAGIADKFNNAKALSYAERFKL 333  
 QY 251 VSSYLAQVRAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNNAKALSYAERFKL 310  
 Db 334 GYEGDLSLAEYQRTGTTIDASTAVNTALAAISGVSAAGSLVGPALILVSGITGII 393  
 QY 311 GYDGNLLAEYQRTGTTIDASTAVNTALAAISGVSAAGSLVGPALILVSGITGVI 370  
 Db 394 STILQYSQAMFEHVANKIHDKVDEKHKNGYFENGYSRVLADLQNNROLQNLK 453  
 QY 371 STILQYSQAMFEHVANKIHKNVWEKKNKNGYFENGYSRVLADLQNNKFLNLK 430  
 Db 454 ELQAEVIRITQQQWNNIGNLAGISRLGKVMGSKAYADAFEEGKLTAKDTFVQLDSAT 513  
 QY 431 ELQAEVIRITQQQWNNIGNLAGISRLGKVMGSKAYADAFEEGKLTAKDTFVQLDSAN 490  
 Db 514 GVINTSKSDNVKTHILPRTPLLPFGVNRRIQTKGYEYITKLNINRVDSSWKITDGA 573  
 QY 491 GIDVSNSSGAKTQHILPRTPLLPFGVNRRIQTKGYEYITKLNINRVDSSWKITDGAAS 550  
 Db 574 STEDLTNNVVRIGELHDHADVTKETKIITANLGDGNDVDYFISGTEVDGGNGLDRVH 633  
 QY 551 STEDLTNNVVRIGELHDHADVTKETKIITANLGDGNDVDYFISGTEVDGGNGLDRVH 610  
 Db 634 YSRDYGALTIDATNESVQSGSYTKRVFETGKALHEVTATOSVLVGSREKIEYRHSNNT 693  
 QY 611 YSRDYGALTIDATNESVQSGSYTKRVFETGKALHEVTATOSVLVGSREKIEYRHSNNO 670

Db 694 OHAGYTTDTLTKSVVEELIGTSRNDIFKSGKFDFAHGGDGVNDINAGNDRFLFGGKGF 753  
 QY 671 HHAGYTTDTLTKSVVEELIGTSRNDIFKSGKFDFAHGGDGVNDINAGNDRFLFGGKGD 730  
 Db 754 IIDGGDDDFIDGGQDDILHGGKNDILCTVKG-GNDSISDSGGNDRLSFADSNLKDLT 812  
 QY 731 ILDGGGDDDFIDGGKNDLHGGKDDIFVHRKGDGNDITDSGDKLSFSDSNLKDLT 790  
 Db 813 FEKVNHLMTNKKVKTIONMFRADYAKTVHNYQATADEKIEIEIIGRGERITSKQI 872  
 QY 791 FEKVKHNLVITNSKKKVTIONMFRADFAKEVPNYKATKDEKIEIEIIGRGERITSKQV 850  
 Db 873 DELIEKKGKIDQSELERIAESSALLKESKFASNLKLYSSAGAFASSNDRVGLGPT 932  
 QY 851 DDLIAGNGKITQDELSKVYDNYELLKHKSNVTNSLKLISVSFAFTSSNDRNVLPAPT 910  
 Db 933 SLYEHT-QSVQFVRAA 947  
 QY 911 SMLDQSLSLQFARG 926  
 RESULT 6  
 ID RT2A\_ACTPL STANDARD; PRT; 956 AA.  
 AC P15377;  
 DT 01-APR-1990 (REL. 14, CREATED)  
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE RTX-II TOXIN DETERMINANT A (APX-IIA) (HEMOLYSIN IIA) (HLY-IIA)  
 DE (CYTOLYSIN IIA) (CLY-IIA).  
 GN APXIIA OR CIVIIA OR HLYIIA OR APXA OR APYC.  
 OS ACTINOBACILLUS PLEUROPEUMONIAE (HAEMOPHILUS PLEUROPEUMONIAE).  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC PASTEURACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SEROTYPE 5;  
 RX MEDLINE; 90126233.  
 RA CHANG Y.-F., YOUNG R., STRUCK D.K.;  
 RL DNA 8:635-647(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;  
 RX MEDLINE; 92040145.  
 RA SMITS M.A., BRIARE J., JANSEN R., SMITH H.E., KAMP E.M.,  
 RA GIELKENS A.L.;  
 RL INFECT. IMMUN. 59:4497-4504(1991).  
 CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A PLEUROPEUMONIAE.  
 CC WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND IS MODERATELY CYTOTOXIC  
 CC FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.  
 CC -!- SUBCELLULAR LOCATION: SECRETED.  
 CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING  
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC  
 CC ACTIVITY (BY SIMILARITY).  
 CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE  
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).  
 CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE  
 CC STRUCTURAL TOXIN).  
 DR EMBL; M30602; G141825; -.  
 DR EMBL; X61111; G38941; -.  
 DR PIR; B33389; B33389.  
 DR PIR; S18853; S18853.  
 DR PROSITE; PS00330; HEMOLYSIN\_CALCIUM; 1.  
 KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;  
 KW TRANSMEMBRANE.  
 FT TRANSMEM 233 256 POTENTIAL.  
 FT TRANSMEM 266 323 POTENTIAL.  
 FT TRANSMEM 361 406 POTENTIAL.  
 FT DOMAIN 719 787 8 X REPEATS, GLY-RICH.  
 FT REPEAT 719 724 1.  
 FT REPEAT 728 733 2.  
 FT REPEAT 737 742 3.  
 FT REPEAT 746 751 4.



311 GYDGNLLAEVQRTGTDASVTAINTALAAAGVSAAGSVIAPALLVSGITGVI 370  
 403 TTILEYKQAMFHVANKVHVRIVWEKK-HNNKYFQGGVDSRLADLQNMKFLINLK 461  
 371 STILOYSQAMFHVANKVHVRIVWEKK-HNNKYFQGGVDSRLADLQNMKFLINLK 430  
 462 ELQAEVVAITQOOWDNOIGDLAISRDTKISSGKAYVDAFEGNTSPSIHYSIDKN 521  
 431 ELQAEVVAITQOOWDNOIGDLAISRDTKISSGKAYVDAFEGNTSPSIHYSIDKN 490  
 522 GIINISNTR-KTOSVLFRTPLTPGSENRERIOEGKNSYITIKLHRIQVDSWTVVGDAS 580  
 491 GIIDVNSGKAKTOHILFRTPLTPGSENRERIOEGKNSYITIKLHRIQVDSWTVVGDAS 550  
 581 SSVDFTNVQRIAVKFDAGNIIESKOTKIIANAGANDNVFVGSSTTVIDGGDHRVH 640  
 551 STFDLTNVQRIAVKFDAGNIIESKOTKIIANAGANDNVFVGSSTTVIDGGDHRVH 610  
 641 YSRGEGALVIDATAETKESYSYKRYVGDGSKALHETIATHQTNVGNREEKIEYRREDDR 700  
 611 YSRGEGALVIDATAETKESYSYKRYVGDGSKALHETIATHQTNVGNREEKIEYRREDDR 670  
 701 FHTGTYTDSLSKVEEIIIGSFQNDIFKGSQFDDVFHGGNGVDITIDGNDGDDHLPFGAGDD 760  
 671 HHAGYTKDLKAVEEIIIGSFQNDIFKGSQFDDVFHGGNGVDITIDGNDGDDHLPFGAGDD 730  
 761 VIDGNGNELLVGGTNDIISGGKNDIYVHKTDGNDSDITDSGQDKLAFSDVNLKDLT 820  
 731 ILDGNGDDFDIDGGKNDIISGGKNDIYVHKTDGNDSDITDSGQDKLAFSDVNLKDLT 790  
 821 FKKYDSSLEIINOKGKVRIGNWFLEDDLASTVANYKATNDRKTEELIIGGGERITSEOV 880  
 791 FEKVYKHLNLTNSKKEKVTQNWFRADFAKEVYNYKATNDRKTEELIIGGGERITSEOV 850  
 881 DKLKEGNNQISAEALSKVNDYTSKDRONVNSLAKLSSVGSFTSSSDFRNNLTYY 940  
 851 DDLAKNGKITDLSKVNDYTSKDRONVNSLAKLSSVGSFTSSSDFRNNLTYY 909  
 941 PSSIDVS-NNIQLARAA 956  
 910 TSMLDQSLSSLOFARGS 926

RESULT 8  
 ID RT32-ACPL STANDARD; PRT; 1052 AA.  
 AC P55131;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE RTX-III TOXIN DETERMINANT A FROM SEROTYPE 8 (APX-III) (CYTOLYSIN III) (CLY-III)  
 GN APXIIIA OR CLYIIIA OR RTX OR PTXA.  
 OS ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTEURACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-405 / SEROTYPE 8;  
 RX MEDLINE; 95012630.  
 RA JANSEN R., BRIARE J., VAN GEEL A.B.M., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;  
 RA SMITS M.A.;  
 RL INFECT. IMMUN. 62:4411-4418(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SEROTYPE 8;  
 RX MEDLINE; 93162836.  
 RA JANSEN R., BRIARE J., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;  
 RA INFECT. IMMUN. 61:947-954(1993).  
 CC -!- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.  
 CC -!- SUBCELLULAR LOCATION: SECRETED.  
 CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING

CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY (BY SIMILARITY).  
 CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).  
 CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).  
 DR EMBL; X80055; G558152; -.  
 DR EMBL; X68815; G38958; -.  
 DR PROSITE; PS00330; HEMOLYSIN\_CALCIUM; 3.  
 KW TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM; TRANSMEMBRANE.  
 FT TRANSMEM 248 265 POTENTIAL.  
 FT TRANSMEM 275 334 POTENTIAL.  
 FT DOMAIN 754 859 7 X REPEATS, GLY-RICH.  
 FT REPEAT 754 759 1.  
 FT REPEAT 763 768 2.  
 FT REPEAT 772 777 3.  
 FT REPEAT 781 786 4.  
 FT REPEAT 790 795 5.  
 FT REPEAT 799 804 6.  
 FT REPEAT 808 813 7.  
 FT REPEAT 827 832 8.  
 FT REPEAT 836 841 9.  
 FT REPEAT 845 850 10.  
 FT REPEAT 854 859 11.  
 SQ SEQUENCE 1052 AA; 112809 MW; 0469F67F CRC32;

Query Match 42.1%; Score 2616; DB 1; Length 1052;  
 Best Local Similarity 52.7%; Pred. No. 0.00e+00;  
 Matches 404; Conservative 178; Mismatches 165; Indels 20; Gaps 17;

Db 55 GNKLVVIP-K-EYDSVNGVGFEDLVKAAEELGIQVYNNRNELEVAHKSLSGTADFGL 112  
 QY 14 AKRIILYQNYQDYEQNGLDLVKAAEELGIQVYNNRNELEVAHKSLSGTADFGL 73  
 Db 113 TERGLTFLPOLQDLQKHKSINNVYSGTSDGAVSKLAKSOTIISGIVSLGVLAGINL 172  
 QY 74 TERGVLSAPQIDKLQK-TKAGQALGSAES-IVQNAKRAKTVLSGIVSLGVLAGMDL 131  
 Db 173 NEAIIISGSELELAAGVSLASSELVSNIAKGTITDAFTQIQNFKLVENAKGLGVGR 232  
 QY 132 DEALQNNNOHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLNKGLTGLD 191  
 Db 233 OLONISGSALSKTGLDIISSLLSGVTASFALANKASTSTKVAAGFELSNOVIGITK 292  
 QY 192 KLNIGG--LDKAGLDIVISGLLSGATAALVLDKNAKSTAKKVGAGFELANQVGNITK 249  
 Db 293 AVSSYILAORLAAGLSTTGPAAALIASSTLSAISPLAFLRVADNENRSKEIGFAERFK 352  
 QY 250 AVSSYILAORLAAGLSTTGPAAALIASSTLSAISPLAFLRVADNENRSKEIGFAERFK 309  
 Db 353 LGYDGLKLSSEFYHEAGTIDASITTSALSAAGTAAASAGALVGPITLTVGTIGL 412  
 QY 310 LGYDGNLLAEYORGITDASVTAINTALAAAGVSAAGSVIAPALLVSGITGV 369  
 Db 413 ISGILEFSKQPMLDHVASKIGNKIDWEKK-YOKNTFENGYDARHKAFLSDSFLSSFN 471  
 QY 370 ISTILOYSQAMFHVANKVHVRIVWEKK-HNNKYFQGGVDSRLADLQNMKFLINL 429  
 Db 472 KOYETERAVLITOORVDEYIGELAGITGDKLSSGKAYVDYFOEGKLLKPKDDFSKVV 531  
 QY 430 KELQAEVVAITQOOWDNOIGDLAISRDTKISSGKAYVDAFEGNTSPSIHYSIDKN 485  
 Db 532 FDPTEKGEIDISNS-QTSTL-LKEVTPLLTPGTSERRTOTGKYEYITKLVKVKDKWVN 589  
 QY 486 LDSANGIIDVNSGKAKTOHILFRTPLTPGSENRERIOEGKNSYITIKLHRIQVDSWTVVGDAS 545  
 Db 590 GVKDKGAVDYTNLQIOHAHS-SSVARGEYREVLRVSHLGNQDKVFLAAGSAEIHAGE 648  
 QY 546 DGAA-SSTFDLTNVQRIAVKFDAGNIIESKOTKIIANAGANDNVFVGSSTTVIDGGDHRVH 604  
 Db 649 GHDVYVYDKTDTGLLVLDGTKATEQGRYSVTRELSATKILREVKNQKSAVKRETTLE 708



364	QY	SGITGVISTILQYSKOAMFEHVANKTHNKIVIEWEKNNHGKNTFENGYDARYLANLQDNMK	423
458	Db	ILSQYNKEYSVERSVLITOOHWDTLIGELAGVTRNGDKTLGSKSYIDYYEEGKRLKKPD	517
424	QY	FLNLANKELQAEARVIAITQQQDNNGITDLAGIRGEKVLGSKAYVDAAEEGKHI--KAD	481
518	Db	EFOKQVDFPLKGNIDLSDS-KSSTL-LKEVTPLLTGPEEIRERROSKGYEYITELLVKG	575
482	QY	KLV-QL-DSANGIIDVNSGKAKTOHILFRTPLTPGTEHREVRVOTGKYEYITKLNIRV	539
576	Db	DKWTVGVQDKGSVYDYSNLIOHASV-----GN-NOYRIRESHIGDGDVKVFTLSAGSA	629
540	QY	DSWKIITDGA--SSTFDLTNVVORIGIELDNAGNVTKETKIIAKLGEQDNNVFGSGTT	598
630	Db	NIYAGKHDDVYDKTDTCLATIDGPKATEAGNYTVTVLGGDVKVLQEVKQEEVSVK	689
599	QY	EIDGGEGYDRVHYSRNGYCALITDAFKEQGSYTVNRVETG-KALHEVTTSTHTALVN	657
690	Db	RTEKTYRSEYETHINGKNLTETDNLYSVEELTGTRADKFFGSKFADIFHGADGDHIE	749
658	QY	REEKIEYRSHNQHHAG-YYT-KOTLKAVEELIGTSHNDIFKSKENDAFNGDGVDTID	715
750	Db	GNQDNRLYDGNKNDLGSNGDDQLYGGDNKLGAGNN-YLN-GGDGDD	800
716	QY	GNQDNRLFGGKDDILDGGNGDDFIDGGKNDLLHGGKDDIFVHRKGDGND	768
RESULT 11			
ID	HLXA_ECOLI	STANDARD:	PRT: 1024 AA.
AC	P08715;		
DT	01-JAN-1988 (REL. 06, CREATED)		
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)		
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)		
DE	HEMOLYSIN, PLASMID.		
GN	HLXA.		
OG	ESCHERICHIA COLI.		
OC	PLASMID PHYL152.		
OC	PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS		
OC	ENTEROBACTERIACEAE.		
CC	(1)		
CC	SEQUENCE FROM N.A.		
CC	RHES J., WELLS W., VOGEL M., GOEBEL W.;		
CC	FEMS MICROBIOL. LETT. 34:1-11(1986).		
CC	-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD		
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY		
CC	DEFINED.		
CC	-!- SUBCELLULAR LOCATION: SECRETED.		
CC	-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BENDING		
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC		
CC	ACTIVITY.		
CC	-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE		
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.		
CC	-!- DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY		
CC	STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF THE		
CC	URINARY TRACT.		
CC	-!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE		
CC	STRUCTURAL TOXIN).		
DR	EMBL: M14107; G150682; -.		
KW	PROSITE; P500330; HEMOLYSIN_CALCIUM; 4.		
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;		
KW	TRANSMEMBRANE; PLASMID.		
FT	TRANSMEM 238 260	POTENTIAL.	
FT	TRANSMEM 288 327	POTENTIAL.	
FT	TRANSMEM 365 411	POTENTIAL.	
FT	DOMAIN 724 870	16 X REPEATS, GLY-RICH.	
FT	REPEAT 724 729	1.	
FT	REPEAT 733 738	2.	
FT	REPEAT 742 747	3.	
FT	REPEAT 751 756	4.	
FT	REPEAT 760 765	5.	
FT	REPEAT 769 774	6.	
FT	REPEAT 778 783	7.	



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FT REPEAT 787 792 8.
FT REPEAT 796 801 9.
FT REPEAT 807 812 10.
FT REPEAT 817 822 11.
FT REPEAT 826 831 12.
FT REPEAT 835 840 13.
FT REPEAT 844 849 14.
FT REPEAT 856 861 15.
FT REPEAT 865 870 16.
SQ SEQUENCE 1024 AA; 110201 MW; 38CE3D51 CRC32;

Query Match 38.3%; Score 2384; DB 1; Length 1024;
Best Local Similarity 48.6%; Pred. No. 0.00e+00;
Matches 376; Conservative 187; Mismatches 181; Indels 29; Gaps 22;

Db 43 RNAGNRLLILPKDYK-G--QGSSNDLVRTADELGIEVQYDEKNGTAITKQVFGTAERKL 99
QY 11 KTGAKKILYIFQNYDYDEQNGLOLVKAAEELGIEVQREERNIATAQSLGTQTA 70
Db 100 IGLTERGVTFAPQDLKLLQYKAGNIGGGAENIGDNLGRAGGILSTFQNLFTALSS 159
QY 71 IGLTERGVLSAPQDLKLLQK-TRGAQLGS-AESIVQNAKAKTVLSIQSILGSVLG 128
Db 160 MKIDELIKKQSGNVSSSELAKASTELINQLVDTVASLNNVNSFSOOLNTLGSVLNT 219
QY 129 MDLDEAL--ONNS-N-OHA-LAKAGLELTNSLIENIANSVKLTDFEIGOISFGSKLQNI 183
Db 220 KHLNGVGNKQLNPLNDITAGLDTVSGILSAISAFILSNADADTRTKAAAGVBLTKV 279
QY 184 KGLTGLDKLKNIGLDKAGLGLVIGLSGATAALVLADKNNAKTKVAGGAFELANQV 243
Db 280 LQNVKGISQYIIAQRAGGLSTSAAGLIASAVTLAISPLSFLSIADKFKRANKIEY 339
QY 244 VGNITKAVSSYIIAQRAGGLSTGPVAAIASTVSLAISPLAFAGIADKFNHAKSLESY 303
Db 340 SORFKKLGVDGSLAAPHKGTGADASTTITVLAHSVSSGISAAATSLVGPVSAIV 399
QY 304 AERFKKLGVDGSLAAPHKGTGADASTTITVLAHSVSSGISAAATSLVGPVSAIV 363
Db 400 GAVTGIIISGILESKQAMPEHVASKMADYIAEWKK-HGKNYFENGYDARHAALFEDNFK 458
QY 364 SGITGVISTILQYSKOAMPEHVANKIHNVKVEKNHGNKYNFENGYDARYLANLQDNMK 423
Db 459 ILSQNKYSVRSVLITQOHHDTLIGELAGVTRNGDKTLSKSIDYIEBKRLKXKD 518
QY 424 FLNLNKLQAEVIAITQQQDNNIGDLAGISRLGEKVLISGKAYVDAAFEKGHI--RAD 481
Db 519 EFQKQVDFPLKGNIDLSDS-KSSTL-LKFTVPLLTGPEIRERROSGKYEYITELLVGV 576
QY 482 KLV-QL-DSANGIIDVNSGKAKTOHILFPLTPTGTEHREVOTGKYEYITKLNIRV 539
Db 577 DRWTKGVODKGVADYDYNLIQHASV-----GN-NOYREIRIESHLGDGDDKVFLSAGSA 630
QY 540 DSKMITDGAA-SSTFDLTNVVORIGELDNAGNVKTKETKIIAKLGEDDNVFVSGT 598
Db 631 NIYAKGHVYVYKTDCTGLIDGTAKTEAGNYTVTRVLGDDGVKQVLEVKVEQSVGK 690
QY 599 EIDGGEYDRVHYSRGNYGALTIDATKETEQGSYTVNREVTG-KALHEVTSHTHALVN 657
Db 691 RTEKTOYRSYETHINGKNLTETDNLVSVLEELIGTTRADKPFSGKFTDIFHCADGDD 750
QY 658 REEKIEYRHSNQHAG-YYT-KDTLKVAEEIIGTSHNDIFKGSFNFADNGDGDVD 715
Db 751 GNDGNDRLYDGNNDTLGSGNGDDQLYGDDGNDKLGIVAGNN-YLN-GGDGDD 801
QY 716 GNDGNDRLYDGNNDTLGSGNGDDQLYGDDGNDKLGIVAGNN-YLN-GGDGDD 768

RESULT 12
ID RT12ACTPL STANDARD; PRT: 1023 AA.
AC P51129;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
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DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE RTX-1 TOXIN DETERMINANT A FROM SEROTYPES 5/10 (APX-1A) (HEMOLYSIN IA)
DE (HLY-1A) (CYTOLYSIN IA) (CLY-1A).
GN APXIA OR CLYIA OR HLYIA.
OS ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13039 / SEROTYPE 10;
RX MEDLINE: 94276858.
RA NAGAI S., YAGIHASHI T., ISHIHAMA A.;
RL MICROB. PATHOG. 15:485-495(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K17 / SEROTYPE 5;
RX MEDLINE: 96401417.
RA CHIN N., FREY J., CHANG C.F., CHANG Y.F.;
RL FEMS MICROBIOL. LETT. 143:1-6(1996).
RN [3]
RP SEQUENCE OF 886-1023 FROM N.A.
RC STRAIN=K17 / SEROTYPE 5;
RX MEDLINE: 93366425.
RA JANSEN R., BRIAIRE J., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;
RL INFECT. IMMUN. 61:3688-3695(1993).
CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7, 8, 12, AND
CC TOTALLY DELETED IN SEROTYPE 3.
CC -1- THE SEQUENCE SHOWN IS THAT OF SEROTYPE 10.
CC -1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL: D16582; G497787; -.
DR EMBL: U04954; G1477457; -.
DR EMBL: X73116; G312215; -.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 2.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 226 256 POTENTIAL.
FT TRANSMEM 297 326 POTENTIAL.
FT TRANSMEM 367 406 POTENTIAL.
FT DOMAIN 722 845 13 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 813 818 10.
FT REPEAT 822 827 11.
FT REPEAT 831 836 12.
FT REPEAT 840 845 13.
FT CONFLICT 210 217 AMPYLTLA -> GNALSNTN (IN REF. 2).
FT CONFLICT 581 581 E -> Q (IN REF. 2).
FT CONFLICT 687 688 TC -> R (IN REF. 2).
FT CONFLICT 1015 1015 F -> L (IN REF. 2).
SQ SEQUENCE 1023 AA; 110129 MW; BD696437 CRC32;

Query Match 36.1%; Score 2244; DB 1; Length 1023;
Best Local Similarity 45.6%; Pred. No. 0.00e+00;
Matches 372; Conservative 202; Mismatches 209; Indels 32; Gaps 27;

Db 39 KQAGQKLLIYPKDYQAST--GSSNDLVKAAEALGIEVHRSKNGTALAKELFGTTEKL 96
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11 KTGAKKILYIPQNYQYDEGGNGLQDLVRAAEELGIEVQREERNNTATQTSIGTIQTA 70
97 LGPSEKIALFAPQDFKLLKNKOKLSKSGSSEALQORLNKTOTALSALQSFGLTAIG 156
71 IGLTERGIVLSAPOIDKLOKT-KAGQALG-SAESIVQNAKAKTVLSIGTSLGVLG 128
157 MDLSDLLRRRREDEDVSGSELAKAGVDLAQALVDNITASATGTVDAFAEOLGKLAMPYLT 216
129 MDLDEALQNSN-OH---A-LAKAGLELTNSLIENIANSVKTLDEFGQEQISQFGSKLQNI 183
217 -ALSGLASKLNNLPDLSLAGPGFQDAVSGILSVSVASPSILSKNDKADAGAKAAAGTETSKI 275
184 KGLGTGLDKLNGGLDKAGLGLDVISGLSLGATAALVLADKNASTAKKVGAGFELANQV 243
276 LGNTGKAVSYIIAQRVAAGLSTTAATGGILGIVSVALAISPLSFLNVADKFERAKOLEQY 335
244 VGNITKAVSVYLAQRVAAGLSSTGPPVAALIASTVSLAISPLAFAGIADRFNHAKSLESY 303
336 SERFKEGYEGDLSLASFYRETGAIEAALTINSVLSAASAGYGAATGSLVGAPVAALV 395
304 AERFKLGYDGNLALBYQGTGTIDASVTAINTALAAGVSAAGSVIASPIALLY 363
396 SAITGILSGILDASKQAFERFVATKLANKIDWEKK-HGKNYFENGYDARHSFAFLDTPE 454
364 SGITGVSTILOYSQAMFHVANKINKIVEKKNHGNKYNFENGYDARYLANLQDNMK 423
455 LLSQYNKEYSVERRVATTOQRWDVNGELAGITRKADAKSGKAYVDFEFGKLLERKDPD 514
424 FLNLNKLQAEVIAITQOOWDNNIGDLAGISRLGKVLSGKAYVDAPEEGKHI-K-AD 481
515 RFDKVVDPLEKIDLSINKT-TL-LKFTIPVPTAGEEIRERKQTKYEMTELFVKGK 572
482 KLVO--LDSANGIIDVNSGAKAKTQHLFTPLTPGTEHRERVQTKYETITKLNINRV 539
573 EKVVVTGVESHNAIYDTNLIQ-LAID-KK-GE-K-ROYTIESHLCKNDRIYLSGSS 626
540 DSWKITDGAA-SSTFDTNVVQRIEIDNAGNVTKEKTIKLAGGEGDNDVFGSGIT 598
627 IVYAGNHGVAYDKTGYLTFDGQSAKAGEYIVTKELKADVKVLYKVTQDISVGK 686
599 EIDGEGYDRVHSRGNYGALTDATKETEQGSYTVNRFEVETG-KALHEVTSHTALVGN 657
687 TCSKLEYROYELSPFELNGIRAKDELHVSVEELIGSNRKDKFGSFTDIFHGAKGDDE 746
658 R-EKIEYRHSN-NQHAGY-Y-TKDTLKAVEEIIGTSHNDIFKSGSFNDAFNGGCGVDT 713
747 IYNGDGHDIYDGDNDVINGGDNHVLGGNGDRLIGGKGN-FLN-GDGDGDELQVF 804
714 IDGNDGNDRLFGGKDDIILGNGGDDFIDGKGNLHGGKGGDIFVHRKGGDNDIITDS 773
805 EGOYNVLGAG-NDILYSGDGTNLFDGCVGNDKI 838
774 DGNKLSFSDSNLKDITFEKVKNHLVITNSKKKV 808

RESULT 13
ID RTII-ACPL STANDARD; PRT; 1023 AA.
AC P51128;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE RTX-1 TOXIN DETERMINANT A FROM SEROTYPES 1/9 (APX-IA) (HEMOLYSIN IA)
DE (HLY-IA) (CYTOLYSIN IA) (CLY-IA).
GN APXIA OR CLYIA OR HLYIA.
OS ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S 4074 / SEROTYPE 1;
RX MEDLINE; 91348945.
RA FREY J., MEIER R., GYGI D., NICOLET J.;

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RL INFECT. IMMUN. 59:3026-3032(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S 4074 / SEROTYPE 1;
RX MEDLINE; 94237497.
RA FREY J., HALDMANN A., NICOLET J., BOFFINI A., PRENTKI P.;
RL GENE 142:97-102(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
RX MEDLINE; 93366425.
RA JANSEN R., BRIARE J., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;
RL INFECT. IMMUN. 61:3688-3695(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-S 4074 / SEROTYPE 1;
RA CHANG Y., WANG Y., CHIN N.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7, 8, 12, AND
CC TOTALLY DELETED IN SEROTYPE 3.
CC -!- THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1.
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL; X52899; G38950; -.
DR EMBL; X68595; G505570; -.
DR EMBL; X73117; G312899; -.
DR EMBL; U05042; G606616; -.
DR PROSITE; PS00330; HEMOLYSIN-CALCIUM; 2.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 226 256 POTENTIAL.
FT TRANSMEM 297 326 POTENTIAL.
FT TRANSMEM 367 406 POTENTIAL.
FT DOMAIN 722 845 13 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 813 818 10.
FT REPEAT 822 827 11.
FT REPEAT 831 836 12.
FT REPEAT 840 845 13.
FT CONFLICT 210 217 AMPYLTLA -> GNALSNT (IN REF. 3 AND 4).
FT CONFLICT 374 374 R -> A (IN REF. 3 AND 4).
FT CONFLICT 562 562 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 687 688 TC -> R (IN REF. 3 AND 4).
SQ SEQUENCE 1023 AA; 110193 MW; 7F21E8E8 CRC32;
Query Match 36.0%; Score 2236; DB 1; Length 1023;
Best Local Similarity 45.5%; Pred. No. 0.00e+00;
Matches 371; Conservative 203; Mismatches 209; Indels 32; Gaps 27;

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Db 39 KQAGQKILYIPKDYQAST--GSSLNDLVKAAEALGIEVHRSEKNTALAKELFGTTEKL 96
QY 11 KTGAKKILYIPQNYQYDEGGNGLQDLVRAAEELGIEVQREERNNTATQTSIGTIQTA 70
Db 97 LGPSEKIALFAPQDFKLLKNKOKLSKSGSSEALQORLNKTOTALSALQSFGLTAIG 156
QY 71 IGLTERGIVLSAPOIDKLOKT-KAGQALG-SAESIVQNAKAKTVLSIGTSLGVLG 128

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Db 157 MDLSDLLRRRRNGEDSGSLAKAGVDLAQLVNDINTASATGTVDAEQLGKLAMPYLFL 216
QY 129 MDLDELALQNNNSN-OH---A-LAKAGLELTNSLTNSVNTTDEFEQISQFSGSLQNI 183
Db 217 -ALSGLAKLNNLPDLSLACPGFDVSGILSVYSASFILSNKDADAGTAAAGIEISTKI 275
QY 184 KGLCTGDKLKNKGGLDKAGLDVLSGLSGATAALVADKNASTAKKVGAGFELANQV 243
Db 276 LGNIGRAVSQYIIIAQRAAGLSTTAATGGLIGSVVALAISPLSFLNVDAKFERAKOLEQY 335
QY 244 VGNITRAVSQYIIIAQRAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESY 303
Db 336 SERFKFGYEGDSILASFRYETGAIEAALTINSVLSARSAGVGAATSGLVGAPVAALV 395
QY 304 AERFKLGGYDGDNLAEYQRTGTIDASVTAINALAAIAGGVSAAGSVIASPIALIV 363
Db 396 SAITGIISGILDASKOAFPRVATKLANIDWEKK-HGKNYFENGYDARHSAFLEDTFE 454
QY 364 SGITGVISTILOYSKQAMFEHVANKHIVWEKNNHKNKNFENGYDARYLANQDNMK 423
Db 455 LLQYNKXSVVERVAITQORWDVNIAGELAGITRKSDTKSGKAYVDFPEEGKLEKEPD 514
QY 424 FLNLNKLQAEVIAITQOQWNNIGDLGAGISRLGKVLGKAYVDAFECKHI-K-AD 481
Db 515 RFDKVPDPLEGKIDISSINKT-TL-LKFTVPVFTAGEIERKQTKGYMTELEVKGK 572
QY 482 KLVQ--LDSANGIIDVNSGKAKTOHILFTPLLTGTETHEHRRVQTKGYEITKLNINRV 539
Db 573 EKWVTVGVSHNAIYDVTNLQ-LAID-KK-GE--K-ROVTIESHGEKNDRIYLSGSS 626
QY 540 DSKWITDGA--STFOLTNVQVIGIELDNAGNWTKEKIIAKLGEEDNVPVSGGT 598
Db 627 IVYAGNHVDVAYDKTDTGYLTFDGSAOKAGEIIVTKELKADVKVLKVKVITQDISVGK 686
QY 599 EIDGEGYDRVHSRNGYALTDATKETEQQSYTVNRFEVG-KALHEVTSHTALVGN 657
Db 687 TCSEKLEIRDYELSPELGNGIRAKDELHVSIEIGSNRDKKFFGSRFTDIFHAKGDDE 746
QY 658 R-BEKIEYRHSN-NQHAGY-Y-TKDTLKAVEEIIIGTSHNDIFKSGFNDAFNGGVDVT 713
Db 747 IYNGDGHILYGDGNDVTHGGDNDHLVGGNGNDRLIGGKGN-FLN-GGGDDDELQVF 804
QY 714 IDGNDGNDRLFGKGGDDLDGNGDDFDGKGNDLHGGKGGDIFVHRKGGDNDIITS 773
Db 805 EGYNVLLGAG-NDILYGSDDGNTLFDGGVGNKI 838
QY 774 DGNDKLSFSDSNLKDLTFEKVKHNLVITNSKKEV 808

RESULT 14
ID HLVA-ACFAC STANDARD; PRT: 1050 AA.
AC P16462;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN.
GN LKTA OR LTA.
OS ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS
OC ACTINOMYCETEMCOMITANS).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JP2;
RX MEDLINE; 89359382.
RA LALLY E.T., GOLUB E.E., KIEBA I.R., TAICHMAN N.S., ROSENBLUM J.,
RA ROSENBLUM J.C., GIBSON C.W., DEMUTH D.R.;
RL J. BIOL. CHEM. 264:15451-15456(1989).
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.ACTINOMYCETEMCOMITANS
CC MIGHT BE A CYTOTOXIN, POSSIBLY THE MEMBRANE-BOUND HEMOLYSIN.
CC -!- SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED OR SECRETED (BY
SIMILARITY).

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CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN AND
CC SOME NON-HUMAN CELLS OF THE MONOMYELOCYTIC LINEAGE.
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL: M27399; G141834; -.
DR PIR: B34345; B34345.
DR HSSP: P04002; 1ATF.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 5.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 339 359 POTENTIAL.
FT TRANSMEM 408 429 POTENTIAL.
FT TRANSMEM 477 501 POTENTIAL.
FT DOMAIN 722 844 14 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 803 808 10.
FT REPEAT 812 817 11.
FT REPEAT 821 826 12.
FT REPEAT 830 835 13.
FT REPEAT 839 844 14.
SQ SEQUENCE 1050 AA; 114194 MW; 995A56CB CRC32;

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Query Match 34.9%; Score 2167; DB 1; Length 1050;
Best Local Similarity 45.8%; Pred. No. 0.00e+00;
Matches 368; Conservative 190; Mismatches 212; Indels 34; Gaps 25;

Db 44 KTG-KKLTLYTPKNYK----KXNGLTALIKAAQKLGIEVYHEGKDPALTINGILTKKL 98
QY 11 KTGAKIILYIPQNYQYDETEGNGLODLVKAEEGLIEVQREERNNTATATSGTIQTA 70
Db 99 LGLTERGUTLFAPELDKWIQGNKHLNSVSGTGNLTAKIDKVKQSVGLTQLAFLATFSGM 158
QY 71 IGLTERGIVLSAPQIDKLLQTKA--GOALGSAESIVQNAKAKTVLSGIQISGLVLAM 129
Db 159 DLDALIKARQGNKNTVDYQAKASNLINELIGTISSTNNVDTFSKQNLKLGALGVK 218
QY 130 DLDEAL---QNNNSN-QHA-LAKAGLELTNSLTENIANSVKTLDEFEQISQFSGKLQNIK 184
Db 219 HFGSGDKLKNLPKLGNGKYGALSGVLSAISALLLANKHADTATKAAAAELTNKVL 278
QY 185 GLGLTGDKLKNIGGLDKAGLDVLSGLLSGATAAVLADKNASTAKKVGAGFELANQV 244
Db 279 GNIGKAITQYIIIAQRAAGLSTGTPVAGLIAVSVLSAISPLSFLGIAKQFDRARMLEYS 338
QY 245 GNITKAVSYIIIAQRAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESYA 304
Db 339 KRFKFGYNGSLLGQFYKNTGIADAATTINTVLSAAGVGAASAGSLVAGPILGLVS 398
QY 305 ERFKKGVDGNDLAEYQRTGTIDASVTAINALAAIAGGVSAAGSVIASPIALIV 364
Db 399 AITSLISILDASKOAVSEHIANOLADKIKAWE-NKYGKNYSENGYDARHSAFLEDSKL 457
QY 365 GITGVISTILOYSKQAMFEHVANKHIVWEKNNHKNKNFENGYDARYLANQDNMK 424
Db 458 FNEUREKTYTENILSITQOQWQDRIGELAGITRNGDRIOGSKAYVDYLKKGEELEAKHSDK 517
QY 425 LLNLNKLQAEVIAITQOQWNNIGDLGAGISRLGKVLGKAYVDAFECKHI-K-ADK 482
Db 518 FTQKLLDPIKGNIDLSGI-KGSTT-LTFLNPLLTAGKEERTQSGKYEFTELKVKGRT 575

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QY 483 LV-Q-LDSANGIIVDSNSGRAKTOHILFRTPLLTGTEHRRVOTGKYEYITKLNIN-RV 539

Db 576 D-NKVKGVPSNGVYDFSNLIQH-AVTRDN--KVL-----EARLIANLGAKDYYVFGSGT 628

QY 540 DSWKITDGAASS-TFDLTNVVQIRIGIELDNAGNVTKTKETKIIAKLGEQDGNVFGSGTT 598

Db 629 IVNAGDGYDVVYDKSGRTGALTIDGRNATKAGQYKVERDLSCGTQVLOETVSKOETRGKV 688

QY 599 EIDGEGGYDRVHSRNGYGALTIDATKETEQSGSYVNRVETSKALHEVTSHTALVGNR 658

Db 689 TDLEERYNKLDYYTNKGFKAHDELSNVEEIIIGSNLRDKFYGSKFNDVPHGHDGDDLIY 748

QY 659 EEKIEYRHSN-NQHA--GYITNDTLKAVEEIIIGTSNDIFKSKFNDAENGDDGVDITD 715

Db 749 GYGDORLYGDNENDEIHGGQGNKLYGGAGNDRLFGEYGN--YLD--GGEGDDHLEGGNG 806

QY 716 GNDGNDRFLFGKGGDDIILGGGDDFIDGKGNLHGGKGGDIFVHRKGGDNDIITDSOG 775

Db 807 SDILRGSGNDK-L-FGNQGGDLL 828

QY 776 NDKLSFSDSNLKDITFEKVHNLV 799

RESULT 15

ID CYAA-BORPE STANDARD; PRT; 1706 AA.

AC P15318; 1

DT 01-APR-1990 (REL. 14, CREATED)

DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE CALMODULIN-SENSITIVE ADENYLATE CYCLASE PRECURSOR (EC 4.6.1.1) (ATP

DE PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE) (BIFUNCTIONAL

DE HAEMOLYSIN-ADENYLATE CYCLASE TOXIN) (CONTAINS: HAEMOLYSIN).

GN CYA OR CYAA.

OS BORDETELLA PERTUSSIS.

OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;

OC ALCALIGENACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=18323;

RX MEDLINE; 88216178.

RA GLASER P., LADANT D., SEZER O., PICHOT F., ULLMANN A., DANCHIN A.;

RL MOL. MICROBIOL. 2:19-30(1988).

RN [2]

RP SEQUENCE OF 1489-1706 FROM N.A., AND BIFUNCTIONAL PROTEIN DESCRIPTION.

RC STRAIN=18323;

RX MEDLINE; 89091151.

RA GLASER P., SAKAMOTO H., BELLALOU J., ULLMANN A., DANCHIN A.;

RL EMBO J. 7:3997-4004(1988).

RN [3]

RP DOMAINS.

RX MEDLINE; 91177021.

RA MUNIER H., GILLES A.-M., GLASER P., DANCHIN A., SARFATI R., BARZU O.;

RL EUR. J. BIOCHEM. 196:469-474(1991).

RN [4]

RP MUTAGENESIS.

RX MEDLINE; 89251630.

RA GLASER P., ELMAOGLU-LAZARIDOU A., KRIN E., LADANT D., BARZU O.,

RA DANCHIN A.;

RL EMBO J. 8:967-972(1989).

RN [5]

RP MUTAGENESIS.

RX MEDLINE; 91266896.

RA GLASER P., MUNIER H., GILLES A.-M., KRIN E., PORUMB T., BARZU O.,

RA SARFATI R., PELLECUER C., DANCHIN A.;

RL EMBO J. 10:1683-1688(1991).

RN [6]

RP REVIEW.

RX MEDLINE; 93119764.

RA DANCHIN A.;

RL ADV. SECOND MESSENGER PHOSPHOPROTEIN RES. 27:109-162(1993).

CC -I- FUNCTION: THIS ADENYLATE CYCLASE BELONGS TO A SPECIAL CLASS OF

CC BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON MAMMALIAN

CC CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DISRUPTS NORMAL

CC CELL FUNCTION.

CC -I- CATALYTIC ACTIVITY: ATP -> 3',5'-CYCLIC AMP + PYROPHOSPHATE.

CC -I- ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.

CC -I- SUBCELLULAR LOCATION: SECRETED.

CC -I- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING

CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC

CC ACTIVITY (BY SIMILARITY).

CC -I- PTM: RELEASED IN A PROCESSED FORM.

CC -I- SIMILARITY: BELONGS TO CLASS-2 OF ADENYLATE CYCLASES.

DR EMBL; Y00545; G396666;

DR EMBL; X14199; G39732;

DR EMBL; A07292; G412231;

DR EMBL; A14850; G580668;

DR PIR; S00893; OYBR.

DR PIR; S09403; S09403.

DR PROSITE; P500330; HAEMOLYSIN CALCIUM; 5.

KW LYASE; CAMP SYNTHESIS; ATP-BINDING; HAEMOLYSIS; TOXIN; VIRULENCE;

KW WHOOPING COUGH; CALCIUM-BINDING; REPEAT.

FT CHAIN 1 312

FT CHAIN 313 1706

FT DOMAIN 1 399

FT DOMAIN 400 912

FT DOMAIN 913 1656

FT DOMAIN 1657 1706

FT NP\_BIND 349 356

FT DOMAIN 913 1610

FT REPEAT 913 918

FT REPEAT 1015 1020

FT REPEAT 1024 1029

FT REPEAT 1033 1038

FT REPEAT 1033 1038

FT REPEAT 1042 1047

FT REPEAT 1051 1056

FT REPEAT 1060 1065

FT REPEAT 1080 1085

FT REPEAT 1155 1170

FT REPEAT 1174 1179

FT REPEAT 1183 1188

FT REPEAT 1203 1208

FT REPEAT 1280 1285

FT REPEAT 1289 1294

FT REPEAT 1298 1303

FT REPEAT 1307 1312

FT REPEAT 1316 1321

FT REPEAT 1325 1330

FT REPEAT 1345 1350

FT REPEAT 1421 1426

FT REPEAT 1430 1435

FT REPEAT 1439 1444

FT REPEAT 1448 1453

FT REPEAT 1556 1561

FT REPEAT 1565 1570

FT REPEAT 1574 1579

FT REPEAT 1583 1588

FT REPEAT 1593 1598

FT REPEAT 1605 1610

FT MUTAGEN 188 188

FT MUTAGEN 190 190

FT MUTAGEN 298 298

FT MUTAGEN 301 301

SO SEQUENCE 1706 AA; 177506 MW; 1CE709AA CRC32;

Query Match 14.4%; Score 896; DB 1; Length 1706;

Best Local Similarity 32.0%; Pred. No. 9.23e-119;

Matches 191; Conservative 165; Mismatches 212; Indels 29; Gaps 26;

Db 530 GGFVAGGAMALGGGIAAAGVAGMSLTD-DAPAGQKAAAGATAIQLTGTVELASSIAL 588

QY 197 GGLDKAGLGLDVTISGLLSGATLALVADNASTAKKVGAGFELANOVGNITKAVSSY-I 255

Db 589 ALAAARGVTSGLVAGASAGAAALAAALSPMEIYGLVQOQSHYADOLKLAQESSAYGY 648

QY 256 -LAQ-R-VAAGLSSTGCPVAALIASTVSLAISPLAFAGIADKFNHAKSNLESYAERFKKLG 312

Db 649 EGDALLAQLYRDKTAAEGAVAGVSAYLSTVGAASVIAAAASVVGAPVAVVTSLLTGALNG 708  
:| | | | : : : : : | : : : : | | | | : : : : | : | : |

QY 313 DGDNLLAEYQRCGTGTIDASVTAINALAAIAGVSAAAAGSVIASPIALLVSGITGVIST 372  
| : : : : | : | : | : | : | : | : | : | : | : | : | : |

Db 709 ILRGVOOPIIEKLANDYARKI-D-ELGGP-QAYFEKNQARHEQLANSDGLRKMILADLOA 765  
| : : : : | : | : | : | : | : | : | : | : | : | : | : |

QY 373 ILQYSKQAMFEHVANKIHKNKIVWEKNNHGNKYNFENGYDARY--LANQDNMKFLLNLNK 430  
| : : : : | : | : | : | : | : | : | : | : | : | : | : |

Db 766 GWNASSVIGVQTEISKSALAAITIGNADNLKSDVDFVDRFVQGERVAGOPVV-LDVAA 824  
| | : : : : : : : : : | : | : | : | : | : | : | : |

QY 431 ELQAEVIAITQQQWNNIGDLAGISRLGKVLGSKAYVDAFECKHAKDLVQLDSAN 490  
| | : : : : : : : : : | : | : | : | : | : | : | : |

Db 825 GGIDIASR-KGERPALFTTPLAAPGEEQRRRTKTKSEFTTFVEIVGKQDRWRIRDGAA 883  
| | : : : : : : : : : | : | : | : | : | : | : | : |

QY 491 GIIDVSNCKAKTQHILFRTPLLTPGTEHRRVQTKGYEYITKLN-IRVDSMKITDGAA 549  
| : : : : | : | : | : | : | : | : | : | : | : | : | : |

Db 884 DTTIDLAKVVSQ-L-VD-AN-G-VLK-HSIKLDVIGGDDVVLANASRIHYDGGAGTNTV 938  
:| | | : | : : : | : | : | : | : | : | : | : | : |

QY 550 SSTFDLTNVQRIGIELDNAGNVTKTKETKIIAKLGEQDDNVFVSGGTTIEDGGEYDRV 609  
| : : : : | : | : | : | : | : | : | : | : | : | : | : |

Db 939 SYAALGRQDSITVSA--DGER--ENVRKOLNNAVYREGVATQTTAYGKRTENVQYRHYVE 994  
| : : : : | : | : | : | : | : : : | : | : | : | : | : |

QY 610 HYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHADVGNREEKIEIRHSN 668  
| : : : : | : | : | : | : | : : : | : | : | : | : | : |

Db 995 LARVGQVVEVDTLHVQHIIGGAGNDSITGNADNFLAGSGGDDRLDGGAGNDTLVGGEG 1054  
: : : : | : | : | : | : | : : : | : | : | : | : | : |

QY 669 NQHHAGYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGDDVTIDGNDGNDRLFGGKG 728  
: : : : | : | : | : | : | : : : | : | : | : | : | : |

Db 1055 QNTVIGGAGDDVFLQDLGVSNQLDGGAGVDVYKNVHQPSEERLERMGDTGIHADL 1111  
: : : | | | : : | : : | | | : : | : : | : : | : : |

QY 729 DDILDGNGDD-FIDG-GKGNLLHGGKG-DDI-F-VHRKGDGN-DIITDSGNDKL 779

\*\*\*\*\*  
WQELH  
(TM)  
\*\*\*\*\*

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:25:49 1998; Maspar time 49.79 Seconds  
Tabular output not generated.  
936.191 Million cell updates/sec

Title: >US-08-455-970-12  
Description: (1-936) from US08455970.pep  
Perfect Score: 6217  
Sequence: 1 MATVIDLSFPKTKAKKILY.....LSSLQFARGSQHWSYGLRPG 936

Scoring table: PAM 150  
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: spiremb6  
1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_phase 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 54.486; Variance 138.232; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	ID	
1	2324	37.4	998	2	Q47461 PLASMID-DNA FOR EHEC-H
2	2321	37.3	998	2	Q47462 HEMOLYSIN.
3	2307	37.1	998	2	P71223 EHEC-HEMOLYSIN.
4	2207	35.5	1055	2	Q43892 LEUKOTOXIN.
5	1758	28.3	758	2	Q46716 HLYA (FRAGMENT).
6	1396	22.5	233	2	Q51865 LEUKOTOXIN A (FRAGMENT
7	1247	20.1	211	2	Q51867 LEUKOTOXIN A (FRAGMENT
8	1208	19.4	208	2	Q51868 LEUKOTOXIN A (FRAGMENT
9	1148	18.5	200	2	Q51866 LEUKOTOXIN A (FRAGMENT
10	887	14.3	1705	2	Q05179 ADENYLATE CYCLASE HEMO
11	493	7.9	181	2	Q70070 ALPHA HEMOLYSIN (FRAGM
12	492	7.9	181	2	Q68403 ALPHA HEMOLYSIN (FRAGM
13	492	7.9	181	2	Q68404 ALPHA HEMOLYSIN (FRAGM
14	272	4.4	219	2	P96437 EXPEL.
15	270	4.3	269	2	Q05199 SLYA PROTEIN.
16	225	3.6	322	2	Q44223 HLYA (FRAGMENT).
17	226	3.6	398	2	Q67179 HEMOLYSIN.
18	221	3.6	835	2	Q56012 CELL-SURFACE-ASSOCIATE
19	224	3.6	937	2	Q44492 MANNURONAN C-5-EPIMERA
20	223	3.6	997	2	Q44495 MANNURONAN C-5-EPIMERA

21	226	3.6	1028	2	O68083 POTENTIAL OUTER MEMBRA	3.58e-13
22	217	3.5	591	2	P73019 IRON-REGULATED PROTEIN	5.48e-12
23	218	3.5	643	2	O68085 HYPOTHETICAL 64.2 KD P	4.05e-12
24	211	3.4	1403	2	Q44494 MANNURONAN C-5-EPIMERA	3.31e-11
25	203	3.3	1741	2	P73817 HEMOLYSIN.	3.56e-10
26	200	3.2	646	2	O51813 OSCILLIN.	8.60e-10
27	198	3.2	1839	2	Q44496 MANNURONAN C-5-EPIMERA	1.54e-09
28	189	3.0	958	2	O33527 BACTERIOCIN.	2.10e-08
29	181	2.9	553	2	Q44493 MANNURONAN C-5-EPIMERA	2.06e-07
30	175	2.8	474	2	Q52515 LIPASE.	1.12e-06
31	169	2.7	465	2	O33680 ENDO-1,3-1,4-BETA-GLYC	5.90e-06
32	167	2.7	613	2	O59933 EXTRACELLULAR LIPASE (	1.02e-05
33	169	2.7	1771	2	P74647 HYPOTHETICAL 192.2 KD	5.90e-05
34	162	2.6	480	2	O69771 SERRALYSIN PRECURSOR (	3.99e-05
35	160	2.6	613	2	O59932 LIPASE (EC 3.1.1.3) (T	6.84e-05
36	164	2.6	1290	2	P74649 LEUKOTOXIN (LTA).	2.32e-05
37	159	2.6	1517	2	O34071 ORF40.	8.95e-05
38	159	2.6	3591	2	O45365 FILAMENTOUS HEMAGGLUTI	8.95e-05
39	156	2.5	272	2	O53085 NODO.	1.99e-04
40	133	2.5	476	2	P72120 ALKALINE PROTEINASE.	4.41e-04
41	148	2.4	834	2	O52647 OUTER MEMBRANE PROTEIN	1.63e-03
42	147	2.4	1361	2	O30524 S-LAYER PROTEIN.	2.11e-03
43	150	2.4	3016	2	P73590 HYPOTHETICAL 311.5 KD	9.69e-04
44	143	2.3	476	2	O66388 METALLOPROTEASE.	5.89e-03
45	135	2.2	999	9	O21882 HYPOTHETICAL 104.5 KD	4.38e-02

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	998 AA.
ID	Q47461	AC	Q47461	
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)		
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998	(TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	PLASMID-DNA FOR EHEC-HEMOLYSIN OPERON.			
GN	EHEC-HLYA.			
OS	ESCHERICHIA COLI.			
OG	PLASMID P0157.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-EDL 933;			
RX	MEDLINE; 95172699.			
RA	SCHMIDT H., BEUTIN L., KARCH H.;			
RL	INFECT. IMMUN. 63:1055-1061(1995).			
DR	EMBL; X86087; E152893;			
DR	PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 2.			
DR	PFAM; PF00353; hemolysinCbind.			
KW	PLASMID.			
SQ	SEQUENCE 998 AA; 107032 MW; 3CCADC38 CRC32;			
Query Match 37.4%; Score 2324; DB 2; Length 998;				
Best Local Similarity 46.9%; Pred. No. 0.00e+00;				
Matches 368; Conservative 199; Mismatches 188; Indels 29; Gaps 23;				
Db	29	RSAGKKLILIPNY--EA-QGVGINELYKADELGIETIHRTERDQTATNQFFGAAEKV	85	
Qy	11	KYCAKKILIIYQNYDYEQNGLDLYKAEELGIEVQREERNIATAQTSLGITQTA	70	
Db	86	VGTERGVAIFAPQLDKLQYKQVKGKIGGTAENYNNLGRAGTVLSALQNTFTIALSG	145	
Qy	71	IGLTERGIVLSAPQIDKLQK-TKGAQALG-SAESIVQNAKAKTVLSGIOSILGSLVAG	128	
Db	146	MALDELLLRQCEDEDSQNDIAKSSIETLNQLVDYTVSSINSTVDSFSEQLNQLGSLSSK	205	
Qy	129	MDLDEAL--QNNNS--N--QHALAKAGLELNTSLIENTANSVKTLDGFEQGISQFGSKLQNI	183	
Db	206	PRLSVGGKLNQLPDLGLGDDGVVSGILSAVSASFILGNSDAHTGTAAAGIELTTOV	265	
Qy	184	KGUGTGLDKLKNIGGLDKAGLDLVISGLLSGATAAVLVADKNASTAKKVGAGFELANQV	243	









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RESULT 8
ID Q51866 PRELIMINARY; PRT; 208 AA.
AC Q51866;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DE LEUKOTOXIN A (FRAGMENT).
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T4 SEROTYPE;
RA LAINSON A.F., AITCHISON K.D., DONACHIE W.;
RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 222885; G311827.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 1.
DR PFAM: PF00353; hemolysinCabin.
FT NON_TER 1
SQ SEQUENCE 208 AA; 22803 MW; A8C5DB0F CRC32;

Query Match 19.4%; Score 1208; DB 2; Length 208;
Best Local Similarity 82.2%; Pred. No. 1.84e-166;
Matches 171; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Db 1 GNDRLFGGKDDIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDK 778
QY 719 GNDRLFGGKDDIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDK 778
Db 61 LSFSDSNLKLDTFKVNHHLVINTKQKVTIQNWFEAEFAKTIYRVATRDKIEEII 120
QY 779 LSFSDSNLKLDTFKVNHHLVINTKQKVTIQNWFEAEFAKTIYRVATRDKIEEII 838
Db 121 GNGERTTSQVDELIEKGGKIDKSDLSQVVDNYQLKYSRDASNSLDKLISSAFTS 180
QY 839 GNGERTTSQVDELIEKGGKIDKSDLSQVVDNYQLKYSRDASNSLDKLISSAFTS 898
Db 181 SNDSRNLVAPTSMLDQSLSLQFARG 208
QY 899 SNDSRNLVAPTSMLDQSLSLQFARG 926

RESULT 9
ID Q51866 PRELIMINARY; PRT; 200 AA.
AC Q51866;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DE LEUKOTOXIN A (FRAGMENT).
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T15 SEROTYPE;
RA LAINSON A.F., AITCHISON K.D., DONACHIE W.;
RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 222886; G311827.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 1.
DR PFAM: PF00353; hemolysinCabin.
FT NON_TER 1
SQ SEQUENCE 200 AA; 21986 MW; 172FA6E4 CRC32;

Query Match 18.5%; Score 1148; DB 2; Length 200;
Best Local Similarity 81.5%; Pred. No. 1.21e-156;
Matches 163; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Db 1 KGGDIIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDKLSFSDSNL 60
QY 727 KGGDIIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDKLSFSDSNL 786
Db 61 KDLTFKVNHLVINTKQKVTIQNWFEAEFAKTIYRVATRDKIEEIIQNGERIT 120
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QY 787 KDLTFKVNHLVINTKQKVTIQNWFEAEFAKTIYRVATRDKIEEIIQNGERIT 846
Db 121 SKOVDELIEKGGKIDKSDLSQVVDNYQLKYSRDASNSLDKLISSAFTSSNDSRNL 180
QY 847 SKQVDDLIAGKNGKITQDELKSVVDNYELKHKSNVTNSLDKLISSAFTSSNDSRNL 906
Db 181 ASPTSMLDPSLSIQFARAA 200
QY 907 VAPTSMLDQSLSLQFARG 926

RESULT 10
ID Q05179 PRELIMINARY; PRT; 1705 AA.
AC Q05179;
DT 01-JUL-1997 (TREMBREL. 04, CREATED)
DT 01-JUL-1997 (TREMBREL. 04, LAST SEQUENCE UPDATE)
DE ADENYLATE CYCLASE HEMOLYSIN.
GN CYAA.
OS BORDETELLA BRONCHISEPTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC ALCALIGENACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CIP 9.73;
RX MEDLINE: 96009899.
RA BETSOU F., SIMEIRO O., DANCHIN A., GUISSO N.;
RL GENE 162:165-166(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CIP 9.73;
RA DANCHIN A.;
RL SUBMITTED (SEP-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CIP 9.73;
RA DANCHIN A.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 237112; E310699.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 4.
DR PFAM: PF00353; hemolysinCabin.
SQ SEQUENCE 1705 AA; 177249 MW; 452163B0 CRC32;
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Query Match 14.3%; Score 887; DB 2; Length 1705;
Best Local Similarity 31.8%; Pred. No. 2.99e-114;
Matches 190; Conservative 165; Mismatches 212; Indels 30; Gaps 27;

Db 530 GFGVAGGAMALGGI-GAVGAGMSLTD-DAPAGQAAAGAEIALQITGGTVELASSIAL 587
QY 197 GGLDKAGLGDVIGSLGATAALVLADKNASTAKKVGAGFELANQVGNITKAVSSY-I 255
Db 588 ALAAARGVTSLQVAGASAGAAALAAALSPMEIYGLVQSHVADQDLKLAQESSAYG 647
QY 256 -LAQ-R-VAAGLSTGFVAAIALASTVSLALSLAPFAGIADKFNHAKSLSYAEFRKLG 312
Db 648 EGDALLAQLYRDKTAEGAVAGYSAVLSVGAASVIAAASVYVAVVYVTSITGALNG 707
QY 313 DGDNLLAEYQRTGTDASVTAINTALAAATAGGVSAAAAGSVIATALLVSGITGVIST 372
Db 708 ILRGVQVQPIIEKLANDYARKI-D-ELGGP-QAYFEKNLQARHEOLANSOGLRMLADLQA 764
QY 373 ILOYSKQAMPEHVANKIHNKIVEWKNHNGKNYFENGIDARY--LANLDQNMKFLNLNK 430
Db 765 GWASSVIGVQTTEIKSALEALATGNADNLKASDVDFVDFIOGERSVAGQPVV-LDVAA 823
QY 431 ELQAEVIAITQQQWNNIGDLGAGISRLGKVLGSKRAYVDFAEEGRHKIKADKLVLQDLSAN 490
Db 824 GGDIASR-KGERPALTFITPLAAPGEEQRRRTKTKGSEFTTFEIVGKQDRWRIRGAA 882
QY 491 GIIDVNSGRKAKTHILFRPTPLTPGTEHREVRQTKYEYITKLN-IRYVDSWKITDGA 549
Db 883 DTTIDLAKVYSQ-LVD-AN-G-VLK-HSILEKVIIGDGDVVLANASRIHVDGAGNTV 937
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Qy	550	SSTFDLNNVVGIGIELDNAGNTYKTKETKIIAKLSEGDNDNVFVSGTWEIDGEGYDRV	609
Db	938	SYAALGRQDSTTVA--DGER--FNVRKQLNNANVREGVATOKTAYGRKTNVQYRHVE	993
Qy	610	HYSR-GNYGALTIDATKETEQSGSYNRFVETGKALHEVTSTHTALVGNREEKIEYRHSN	668
Db	994	LARYGQLVVEVDTEHVGHIHTGGAGNDSITGNAHDNFLAGGAGDRLDGGAGNDTTLVGGS	1051
Qy	669	NOHHAGYYTKDTLKAIVEIIGTSHNDLFFKSKGNDAFNGGVDYTDGNDGNDRLFGGKG	728
Db	1054	HNTVVGGAGDDVFLDLDGVVSNOLDGGAGYDVTWKYNVHOPSEERLERMGDTGTHADL	1110
Qy	729	DDILDGGNGDD-FDYG-GKGNLDLHGKGK-GDDI-F-VHRKGDGN-DIITDSGNDKRL	779

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RESULT 11
ID 070070 PRELIMINARY; PRT; 181 AA.
AC 070070;
AD 070070;
DT 01-AUG-1998 (TREMBREL. 07, CREATED)
DT 01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE ALPHA HEMOLYSIN (FRAGMENT).
GN HYL.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ECOR 48, ECOR 51, ECOR 52, ECOR 54, ECOR 60, ECOR 63;
RA BOYD E.F., HARTL D.L.;
RL J. BACTERIOL. 180:1159-1165(1998).
DR ENBL; AF037579; G2952258; -
DR ENBL; AF037574; G2952248; -
DR ENBL; AF037575; G2952250; -
DR ENBL; AF037576; G2952252; -
DR ENBL; AF037577; G2952254; -
DR ENBL; AF037578; G2952256; -
FT NON_TER 1
SQ SEQUENCE 181 AA; 19104 MW; 47980826 CRC32;

```

Query Match	7.9%	Score 493;	DB 2;	Length 181;
Best Local Similarity	46.4%;	Pred. NO. 5.26e-52;		
Matches	84;	Conservative	44;	Mismatches 46;
			Indels	7;
			Gaps	6;
Db	1	GSSLNDVRRADELGIEVQYDEKNGTATITKQVFCTAEKLGITGRTGVTFAPOLDKLQK	60	
Qy	32	GNGLQDLVKAEEELGIEVQREERNITATQSLGTLQALGRTGIVLSPAQIDKLQK	91	
Db	61	YQKAGNKLGGSAENIGDNLGKAGSVLTFQNLGTALSSMKIDELIKKQSGSNVSSEL	120	
Qy	92	-TKAQALG-SAESIVQNANKAKTVLSGQISLGSVLGAGMDLDEAL--QNN-SN-QHA-L	144	
Db	121	AKASIELINOLVDVTAASINNNVNSFSQOLNKLGSVLNTHKLVNGVGNKLNLPNLNIGA	180	
Qy	145	AKAGELTNSLIENIANSVKTLDEFGQISQFQSGKQNIKRGTLTGDKLKNIGGLDKAGL	204	
Db	181	G	181	
Qy	205	G	205	

RESULT	12	PRELIMINARY;	PRT;	181 AA.
ID	O68403			
AC	O68403;			
DT	01-AUG-1998	(TREMREL. 07, CREATED)		
DT	01-AUG-1998	(TREMREL. 07, LAST SEQUENCE UPDATE)		
DT	01-AUG-1998	(TREMREL. 07, LAST ANNOTATION UPDATE)		
DE	ALPHA HEMOLYSIN (FRAGMENT).			
GN	HYLA			
OS	ESCHERICHIA COLI.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	ENTEROBACTERIACEAE.			

RN	[1]	SEQUENCE FROM N.A.
RP		STRAIN=ECOR 24;
RC		BOVD E.F., HARTL D.L.;
RJ		J. BACTERIOL. 180:1159-1165(1998).
RL		ENBL; AF037572; G2952244; -.
DR		NON_TER 1
FT		SEQUENCE 181 AA; 19071 MW; FE43C98B CRC32;
SQ		

Query Match 7.9%; Score 492; DB 2; Length 181;  
Best Local Similarity 45.9%; Pred. NO. 7.48e-52;  
Matches 83; Conservative 45; Mismatches 46; Indels 7; Gaps 5;

Db	1	GSSNDLVRTADELGLIEVQYDEKNGTNAITKQVETGAELKLGILTERGVAIFAPOLDKLLQK	60
Qy	32	NGIQLDVKAAEEGLIEVQREERNITAAOTSLGTIQTALGLTERGIVLSAPOIDLKLLQK	91
Db	61	YQAGNKLGGSAENIGNLGKAGSVLSTFONELGAAALSSMKIDELIKKQKSGNNVSSSEL	120
Qy	92	-TKAQALG-SAESIVGNANKATVLSGIGSIQSLGVLAGMDLDEAL--QNNMQ--HA-L	144
Db	121	AKASIELINOLVDTAAASINNANNVSFSQOLKNLGSVLSNTKHLNGVGNKLNQNLPLDNIGA	180
Qy	145	AKACLELTNSLIENIANSVYTLDEFEQIQISQFQSKLQNIKGLTGLDGKLANIGLQKAGL	204
Db	181	G 181	
Qy	205	G 205	

RESULT 13  
ID O68404 PRELIMINARY; PRT; 181 AA.

AC O68404;  
 DT 01-AUG-1998 (TREMREL. 07, CREATED)  
 DT 01-AUG-1998 (TREMREL. 07, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMREL. 07, LAST ANNOTATION UPDATE)  
 DE ALPHA HEMOLYSIN (FRAGMENT).  
 GN HYL.  
 OS ESCHERICHIA COLI.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.

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OC   ENTEROBACTERIACEAE.
FN   [1]
RN   SEQUENCE FROM N.A.
RP   STRAIN=ECOR 43;
RC   BOYD E.F., HARTL D.L.;
RL   J. BACTERIOL. 180:1159-1165(1998) .
DR   ENBL: AF037573; G2952246; -.
FT   NON_TER_1
SQ   SEQUENCE 181 AA; 19101 MW; 56A4EE22 CRC32;

Query Match      7.9%  Score 492;  DB 2;  Length 181;
Best Local Similarity 45.9%;  Pred. No. 7.48e-52;
Matches 83;  Conservative 45;  Mismatches 46;  Indels 7;  Gaps 5;

```

Db	1	GSSLNDLVRTADELGI	VEYVDKNGTAIT	KQVFGTAELK	LIGLTERGVA	TFAPOLDKLLQK	60
Qy	32	GNGLQDLVKA	EELGIEVQREERN	NTAOTS	LGITQTAIGL	TERGIVLSAPQIDKLLQK	91
Db	61	YQKAGNLGGS	AEINIGNLGK	AGSVLSTF	ONFGLTAL	SSMKIDELIKKQSGNNVSSSEL	120
Qy	92	-TKAQALG-	SAESIVQNA	KAKTIVSG	IOSILGSL	AGMDLDEAL--QNN\$Q--HA-L	144
Db	121	AKASIELINQ	LVDTAASINN	NVNSF	SOQLNKL	GSVLSNTHKLVNGVGNKLNQNLONIGA	180
Qy	145	AKAGLELT	NSLIENIAN	SVKLTDFE	GFGEQISQ	FGSKLQNIKGLGTGLGDKLNIGGLDKAGL	204
Db	181	G	181				
Qy	205	G	205				

RESULT 14  
ID P96437 PRELIMINARY; PRT; 219 AA.

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AC P96437;
DT 01-MAY-1997 (TREMBREL. 03, CREATED)
DT 01-MAY-1997 (TREMBREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE EXPIL.
OS SINORHIZOBIIUM MELILOTI.
OC EUBACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE;
OC SINORHIZOBIIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM2011;
RX MEDLINE; 97175570.
RA BECKER A., RUEBERG S., KUESTER H., ROXLAU A.A., KELLER M., IVASHINA T.,
RA CHENG H., WALKER G.C., PUEHLER A.;
RL J. BACTERIOL. 179:1375-1384(1997).
DR EMBL; Z79692; E263873; -.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
DR PFAM; PF00353; hemolysinCabin.
SQ SEQUENCE 219 AA; 22116 MW; A6EF047F CRC32;

Query Match 4.4%; Score 272; DB 2; Length 219;
Best Local Similarity 46.5%; Pred. No. 2.02e-19;
Matches 47; Conservative 21; Mismatches 32; Indels 1; Gaps 1;

Db 63 GTDVLGNGNDILVGGSGDDLIYGGNGNDILAGAGSDFLLGGRGNDVLLGGAGNDVID 122
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
683 AVEIIGTSHNDIFGKSKNFDAFNGGVDVTIDGNDGNDRFLFGKGGDDILDGGNGDDFID 742
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 GGASDLLAGGSGSDFVFDGGGGNDVILDFTPGEDVLQIS 163
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
743 GKGNDLLHGGKGGDDIFVHRKGDGNDIITD-SDGNDKLSFS 782
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID O05199 PRELIMINARY; PRT; 269 AA.
AC O05199;
DT 01-JUL-1997 (TREMBREL. 04, CREATED)
DT 01-JUL-1997 (TREMBREL. 04, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE SLYA PROTEIN.
GN SLYA.
OS SINORHIZOBIIUM MELILOTI.
OC EUBACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE;
OC SINORHIZOBIIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EFB1;
RA LLORET J., WULFF B.B.H., RUBIO J.M., DOWNIE J.A., BONILLA I.,
RA RIVILLA R.;
RL APPL. ENVIRON. MICROBIOL. 64:1024-1028(1998).
DR EMBL; Y08703; E293909; -.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
DR PFAM; PF00353; hemolysinCabin.
SQ SEQUENCE 269 AA; 27870 MW; 6FC23DBA CRC32;

Query Match 4.3%; Score 270; DB 2; Length 269;
Best Local Similarity 46.5%; Pred. No. 3.84e-19;
Matches 46; Conservative 22; Mismatches 29; Indels 2; Gaps 2;

Db 115 DVLHGENGDVLYGGSGDDLIYGGNGNDILVGGAGSDFLLGGRGNDVLLGGAGNDVIDGG 174
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
686 EII-TGSHNDIFGKSFNDAFNGGVDVTIDGNDGNDRFLFGKGGDDILDGGNGDDFIDGG 744
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 SGSDLLAGGSGSDFVFDGGGGNDVILDFTPGEDVLQIS 213
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
745 KGNDLLHGGKGGDDIFVHRKGDGNDIITD-SDGNDKLSFS 782
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: Wed Dec 9 19:30:04 1998  
Job time : 255 secs.



\*\*\*\*\*  
M A E R L H  
(TM)  
\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:30:22 1998; MasPar time 10.01 Seconds  
Tabular output not generated. 661.729 Million cell updates/sec

Title: >US-08-455-970-12  
Description: (1-936) from US08455970.pep  
Perfect Score: 6217  
Sequence: 1 MATVIDLSFPRKTGAKKILY.....LSSLQFARGSOHWSYGLRPG 936

Scoring table: PAM 150  
Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5\_COMB 2:PCT9\_COMB 3:backfiles1

Statistics: Mean 34.902; Variance 201.135; scale 0.174

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	6217	100.0	936	1	US-08-455-Sequence 12, Applicati	0.00e+00
2	6217	100.0	977	1	US-08-387-Sequence 8, Applicatio	0.00e+00
3	6135	98.7	1069	1	US-07-777-Sequence 9, Applicatio	0.00e+00
4	6135	98.7	1069	1	US-08-170-Sequence 4, Applicatio	0.00e+00
5	6128	98.6	926	3	5476657-3 Patent No. 5476657.	0.00e+00
6	6128	98.6	926	1	US-08-387-Sequence 6, Applicatio	0.00e+00
7	6128	98.6	926	1	US-07-908-Sequence 2, Applicatio	0.00e+00
8	6128	98.6	926	1	US-08-455-Sequence 2, Applicatio	0.00e+00
9	6128	98.6	943	1	US-08-455-Sequence 10, Applicati	0.00e+00
10	6128	98.6	951	1	US-08-455-Sequence 14, Applicati	0.00e+00
11	6057	97.4	1098	1	US-08-170-Sequence 2, Applicatio	0.00e+00
12	6057	97.4	1098	1	US-07-777-Sequence 7, Applicatio	0.00e+00
13	4925	79.2	934	1	US-08-215-Sequence 80, Applicatio	0.00e+00
14	2566	41.3	1244	2	PCT-US93-1 Sequence 2, Applicatio	6.12e-178
15	2239	36.0	544	1	US-08-387-Sequence 10, Applicati	1.35e-153
16	2167	34.9	1403	1	US-07-908-Sequence 3, Applicatio	3.06e-148
17	2167	34.7	1334	3	5476657-1 Patent No. 5476657.	1.01e-147
18	1758	28.3	758	1	US-08-258-Sequence 2, Applicatio	7.08e-118
19	1758	28.3	758	1	US-08-526-Sequence 2, Applicatio	7.08e-118
20	896	14.4	1489	3	PCT-US95-0 Sequence 2, Applicatio	7.08e-118
21	896	14.4	1489	3	5183745-2 Patent No. 5183745.	2.18e-54
22	896	14.4	1794	3	5183745-6 Patent No. 5183745.	2.18e-54
23	160	2.6	613	1	US-08-272-Sequence 3, Applicatio	1.23e-02

24	140	2.3	20	3	5476657-6	Patent No. 5476657.	2.07e-01
25	140	2.3	20	1	US-07-908-Sequence 5, Applicatio	Sequence 5, Applicatio	2.07e-01
26	140	2.3	20	1	US-07-777-Sequence 4, Applicatio	Sequence 4, Applicatio	2.07e-01
27	140	2.3	20	1	US-08-170-Sequence 6, Applicatio	Sequence 6, Applicatio	2.07e-01
28	133	2.1	1536	1	US-08-302-Sequence 2, Applicatio	Sequence 2, Applicatio	5.44e-01
29	133	2.1	1536	1	US-08-038-Sequence 2, Applicatio	Sequence 2, Applicatio	5.44e-01
30	133	2.1	2035	1	US-08-393-Sequence 5, Applicatio	Sequence 5, Applicatio	5.44e-01
31	133	2.1	2035	2	PCT-US93-1Sequence 5, Applicatio	Sequence 5, Applicatio	5.44e-01
32	133	2.1	2035	1	US-08-046-Sequence 5, Applicatio	Sequence 5, Applicatio	5.44e-01
33	133	2.0	1026	1	US-08-194-Sequence 7, Applicatio	Sequence 7, Applicatio	2.12e+00
34	119	1.9	341	1	US-08-062-Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
35	119	1.9	341	2	PCT-US94-0Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
36	119	1.9	341	1	US-08-891-Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
37	119	1.9	341	2	PCT-US96-0Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
38	117	1.9	433	1	US-07-661-Sequence 2, Applicatio	Sequence 2, Applicatio	4.73e+00
39	110	1.8	230	1	US-08-118-Sequence 3, Applicatio	Sequence 3, Applicatio	1.19e+01
40	113	1.8	730	1	US-07-845-Sequence 5, Applicatio	Sequence 5, Applicatio	8.03e+00
41	113	1.8	730	1	US-07-846-Sequence 5, Applicatio	Sequence 5, Applicatio	8.03e+00
42	106	1.7	37	1	US-08-446-Sequence 15, Applicati	Sequence 15, Applicati	2.00e+01
43	105	1.7	572	1	US-07-609-Sequence 6, Applicatio	Sequence 6, Applicatio	2.27e+01
44	105	1.7	572	1	US-08-765-Sequence 6, Applicatio	Sequence 6, Applicatio	2.27e+01
45	107	1.7	746	2	PCT-US95-1Sequence 2, Applicatio	Sequence 2, Applicatio	1.75e+01

ALIGNMENTS

RESULT 1  
ID US-08-455-970A-12 STANDARD; PRT; 936 AA.  
AC xxxxxx  
XX  
DT  
XX  
DE Sequence 12, Application US/08455970A  
XX  
CC Sequence 12, Application US/08455970A  
CC Patent No. 5708155  
CC GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.  
CC APPLICANT: REDMOND, MARK J.  
CC APPLICANT: HUGHES, HUW P.A.  
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
CC TITLE OF INVENTION: CHIMERAS  
CC NUMBER OF SEQUENCES: 15  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION NUMBER: US/08/455,970A  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960,932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 12:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 936 amino acids





QY 181 QNKGTLGDKLKNIGGLDQAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240  
Db 241 NOVVGNTTKAVSSYILAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300  
QY 241 NOVVGNTTKAVSSYILAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300  
Db 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAGGVSAAAGSVIASPIA 360  
QY 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAGGVSAAAGSVIASPIA 360  
Db 361 LLYSGITGVISTILQYSKQAMFEHVANKIHNVKIVVEKNHGNKYPFNGYDARYLANLQD 420  
QY 361 LLYSGITGVISTILQYSKQAMFEHVANKIHNVKIVVEKNHGNKYPFNGYDARYLANLQD 420  
Db 421 NMKFLNLNKLQEAERVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGHKA 480  
QY 421 NMKFLNLNKLQEAERVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGHKA 480  
Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPTGTEHRRVOTGKYETITKLNINRVD 540  
QY 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPTGTEHRRVOTGKYETITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDNGNVTKTETKIIAKLGEQDNNVFGSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDNGNVTKTETKIIAKLGEQDNNVFGSGTTEI 600  
Db 601 DGEGYDRVHYSRGNYGALITDATKETEQSGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
QY 601 DGEGYDRVHYSRGNYGALITDATKETEQSGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
Db 661 KIEVRHNNHAGYYTKDTLKAVEELIGTSHNDIFKGSKFNDFAFGDGVDTIDGNDGN 720  
QY 661 KIEVRHNNHAGYYTKDTLKAVEELIGTSHNDIFKGSKFNDFAFGDGVDTIDGNDGN 720  
Db 721 DRFLGGGDDIILDGNGDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780  
QY 721 DRFLGGGDDIILDGNGDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780  
Db 781 FSDNLKDLTFEKKVKNLVTNNSKKEKVTIONWFREADFAKEVPNYKATKDEKIEEIIQG 840  
QY 781 FSDNLKDLTFEKKVKNLVTNNSKKEKVTIONWFREADFAKEVPNYKATKDEKIEEIIQG 840  
Db 841 NGERITSQVDDLLAKNGKITODELSKVVDNYELLKHSKNVNSLKLSSVSFAFTSSN 900  
QY 841 NGERITSQVDDLLAKNGKITODELSKVVDNYELLKHSKNVNSLKLSSVSFAFTSSN 900  
Db 901 DSRNLVAPTSMLDQSLSSQLQFARGSQHWSYGLRPG 936  
QY 901 DSRNLVAPTSMLDQSLSSQLQFARGSQHWSYGLRPG 936

RESULT 3  
ID US-07-777-715-9 STANDARD: PRT; 1069 AA.  
XX xxxxxx  
XX

Sequence 9, Application US/0777715

Sequence 9, Application US/0777715

Patent No. 5273889

GENERAL INFORMATION:

APPLICANT: Potter, Andrew

APPLICANT: Campos, Manuel

APPLICANT: Hughes, Huw P.A.

TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND

TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 545 Middlefield Road, Suite 200

CITY: Menlo Park

CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94025  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent in Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/777.715  
CC FILING DATE: 19911016  
CC CLASSIFICATION: 424  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 29310-2001320  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-327-7250  
CC TELEFAX: 415-327-2951  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 9:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1069 amino acids  
CC TYPE: AMINO ACID  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1069 AA; 116205 MW; 5591501 CN;  
  
Query Match 98.7%; Score 6135; DB 1; Length 1069;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 1 MATVIDLSPFKTGAKKIIILYIPONYQYDTEQNGLDLVKAAEELGIEVQREERNIATA 60  
Db 61 QTSLGITQIATIGTERGIVLSAPQIDKLLQKTKAGALGSAESIVONANKAKTVLSGIQS 120  
QY 61 QTSLGITQIATIGTERGIVLSAPQIDKLLQKTKAGALGSAESIVONANKAKTVLSGIQS 120  
Db 121 ILGSLVAGMDLDELQNNNSQHALAKAGLELTNSLIENTANSVKTLDGEQEQISQFGSKL 180  
QY 121 ILGSLVAGMDLDELQNNNSQHALAKAGLELTNSLIENTANSVKTLDGEQEQISQFGSKL 180  
Db 181 QNTKLGITLGDKLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240  
QY 181 QNTKLGITLGDKLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240  
Db 241 NOVVGNTTKAVSSYILAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300  
QY 241 NOVVGNTTKAVSSYILAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300  
Db 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAGGVSAAAGSVIASPIA 360  
QY 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAGGVSAAAGSVIASPIA 360  
Db 361 LLYSGITGVISTILQYSKQAMFEHVANKIHNVKIVVEKNHGNKYPFNGYDARYLANLQD 420  
QY 361 LLYSGITGVISTILQYSKQAMFEHVANKIHNVKIVVEKNHGNKYPFNGYDARYLANLQD 420  
Db 421 NMKFLNLNKLQEAERVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGHKA 480  
QY 421 NMKFLNLNKLQEAERVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGHKA 480  
Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPTGTEHRRVOTGKYETITKLNINRVD 540  
QY 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPTGTEHRRVOTGKYETITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDNGNVTKTETKIIAKLGEQDNNVFGSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDNGNVTKTETKIIAKLGEQDNNVFGSGTTEI 600  
Db 601 DGEGYDRVHYSRGNYGALITDATKETEQSGSYTVNRFVETGKALHEVTSTHTALVGNREE 660

QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEAGSYVNRFEVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIGNDGN 720  
QY 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIGNDGN 720  
Db 721 DRLFGGKGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDKLS 780  
QY 721 DRLFGGKGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDKLS 780  
Db 781 FSDSNLKDITFEKVKNHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
QY 781 FSDSNLKDITFEKVKNHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
Db 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900  
QY 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900  
Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927  
QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927

RESULT 4  
ID US-08-170-126-4 STANDARD; PRT: 1069 AA.

AC xxxxxx

Sequence 4, Application US/08170126

Sequence 4, Application US/08170126

Patent No. 5594107

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW

APPLICANT: CAMPOS, MANUEL

APPLICANT: HUGHES, HUW P.A.

TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/170,126

FILING DATE: 20-DEC-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/777,715

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9000-0013.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1069 amino acids

TYPE: amino acid

CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 1069 AA; 116205 MW; 5591501 CN;  
Query Match 98.7%; Score 6135; DB 1; Length 1069;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 1 MATVIDLSFPKGTAKKIIYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIATA 60  
Db 61 QTSLGITQATGLPERGIVLSAPQIDKLLQTKAQOALGSAESIVQNAKAKTVLSGITS 120  
QY 61 QTSLGITQATGLPERGIVLSAPQIDKLLQTKAQOALGSAESIVQNAKAKTVLSGITS 120  
Db 121 ILGSLAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEFGQISQFGSKL 180  
QY 121 ILGSLAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEFGQISQFGSKL 180  
Db 181 QNIKGLGTGLDKKNIGGLDKAGLDVIGSLGATAAALVADKNASTAKKVGAGFELA 240  
QY 181 QNIKGLGTGLDKKNIGGLDKAGLDVIGSLGATAAALVADKNASTAKKVGAGFELA 240  
Db 241 NOVGNITKAVSSYILAQRVAAGLSSTGPAALIASTVSLAISPLAFAGIADKFHAKSL 300  
QY 241 NOVGNITKAVSSYILAQRVAAGLSSTGPAALIASTVSLAISPLAFAGIADKFHAKSL 300  
Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTDASVTANTALAAIAGGVSAAGSVIASPIA 360  
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTDASVTANTALAAIAGGVSAAGSVIASPIA 360  
Db 361 LLVSGITGVISTILOYSKOAMFEHVANKIHKNKIVWEKNNHGNKYNFYENGIDARYLANLQD 420  
QY 361 LLVSGITGVISTILOYSKOAMFEHVANKIHKNKIVWEKNNHGNKYNFYENGIDARYLANLQD 420  
Db 421 NMKFLNLNKLQAEVTAITQQQWDNIGDLAGLSRIGELGKVLGKAYVDAFEKGKHKA 480  
QY 421 NMKFLNLNKLQAEVTAITQQQWDNIGDLAGLSRIGELGKVLGKAYVDAFEKGKHKA 480  
Db 481 DKLVLDSANGIIDVNSGKAKTQHILFPLTPTGTEHRRVQTKYEYITKLNINRVD 540  
QY 481 DKLVLDSANGIIDVNSGKAKTQHILFPLTPTGTEHRRVQTKYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETIIAKLGEEDDNVFGSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETIIAKLGEEDDNVFGSGTTEI 600  
Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEAGSYVNRFEVETGKALHEVTSHTALVGNREE 660  
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEAGSYVNRFEVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIGNDGN 720  
QY 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIGNDGN 720  
Db 721 DRLFGGKGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDKLS 780  
QY 721 DRLFGGKGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITSDGNDKLS 780  
Db 781 FSDSNLKDITFEKVKNHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
QY 781 FSDSNLKDITFEKVKNHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
Db 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900  
QY 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900  
Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927  
QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927

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RESULT 5
ID 5476657-3 STANDARD: PRT; 1003 AA.
XX
AC xxxxxx
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DE 01-JAN-1900
DE
XX Patent No. 5476657.
XX
CC Patent No. 5476657
CC APPLICANT: POTTER, ANDREW A.
CC TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN
CC COMPOSITIONS AND USES THEREOF
CC NUMBER OF SEQUENCES: 8
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/15,537
CC FILING DATE: 09-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 504,850
CC FILING DATE: 05-APR-1990
CC APPLICATION NUMBER: 335,018
CC FILING DATE: 07-APR-1989
CC SEQ ID NO:3:
CC LENGTH: 926
CC SEQUENCE 1003 AA; 107828 MW; 5444703 CN;

Query Match 98.6%; Score 6128; DB 3; Length 926;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDTGQNGLDLVKAAEELGIEVOREERNIATA 60
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Db 61 QTSLGTTIQTATIGLTERGIVLSAPOIDKLLQKTAKAGALGSAESTIVQANKAKTVLSGIQS 120
QY 61 QTSLGTTIQTATIGLTERGIVLSAPOIDKLLQKTAKAGALGSAESTIVQANKAKTVLSGIQS 120

Db 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEFGESIQSGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEFGESIQSGSKL 180

Db 181 QNKGGLGTGDKKNIGGLDKAGLDGVISGLLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNKGGLGTGDKKNIGGLDKAGLDGVISGLLSGATAALVLADKNASTAKKVGAGFELA 240

Db 241 NOVYGNITKAVSSYILAORVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVYGNITKAVSSYILAORVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300

Db 301 ESYAERFKKLGVDGNLLAEYQRTGTIDASVTAINALAAIAGVSAAGSIAPIA 360
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTIDASVTAINALAAIAGVSAAGSIAPIA 360

Db 361 LVSIGITGVISTILQYSKOAMFEHVANKIHNKIYEWKNNHKNYFENGVDARYLANLQD 420
QY 361 LVSIGITGVISTILQYSKOAMFEHVANKIHNKIYEWKNNHKNYFENGVDARYLANLQD 420

Db 421 NMKFLNLLNKLQEAERVIAITQQQMDNNGIDLAGISRLGERKVLGSKAYVDAFEESKHKA 480
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QY 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLTPGTHREHVRVOTGKYEYITKLNINRVD 540

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Db 601 DGGEGYDRVHYSRNGYALTTIDATKETEQSGSYTNRFVETGKALHEVTSHTALVGNREE 660
QY 601 DGGEGYDRVHYSRNGYALTTIDATKETEQSGSYTNRFVETGKALHEVTSHTALVGNREE 660

661 KIEYRHSNNQHHAGYYTKDTLKAVEEIIIGTSHNDIFKSGKFNDAFNGGVDGVDITDGN 720
661 KIEYRHSNNQHHAGYYTKDTLKAVEEIIIGTSHNDIFKSGKFNDAFNGGVDGVDITDGN 720
721 DRLFGGKGGDDILDGNGDDDFIDGGKGNLDLHGGKGGDDIFVHRKGGDNDIITDSDGNDKLS 780
721 DRLFGGKGGDDILDGNGDDDFIDGGKGNLDLHGGKGGDDIFVHRKGGDNDIITDSDGNDKLS 780
781 FSDSNLKDLTFFEKVKHNLVITNSKKEKVITQNFREADFAKEVPNTKATKDEKIEEIIIG 840
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841 NGERITSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
841 NGERITSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
901 DSRNVLVAPTSMLDQSLSLQFARGS 926
901 DSRNVLVAPTSMLDQSLSLQFARGS 926

RESULT 6
ID US-08-387-156-6 STANDARD: PRT; 926 AA.
XX
AC xxxxxx
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DE
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XX Sequence 6, Application US/08387156
XX
XX Sequence 6, Application US/08387156
XX Patent No. 5723129
XX
XX GENERAL INFORMATION:
XX APPLICANT: POTTER, ANDREW A.
XX APPLICANT: REDMOND, MARK J.
XX APPLICANT: HUGHES, HUW P.A.
XX TITLE OF INVENTION: GBRH-LEUKOTOXIN CHIMERAS
XX NUMBER OF SEQUENCES: 28
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: REED & ROBINS
XX STREET: 635 BRYANT STREET
XX CITY: PALO ALTO
XX STATE: CALIFORNIA
XX COUNTRY: UNITED STATES OF AMERICA
XX ZIP: 94301
XX
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/387,156
XX FILING DATE: 10-FEB-1995
XX CLASSIFICATION: 424
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 07/960,932
XX FILING DATE: 14-OCT-1992
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 07/779,171
XX FILING DATE: 16-OCT-1991
XX ATTORNEY/AGENT INFORMATION:
XX NAME: ROBINS, ROBERTA L.
XX REGISTRATION NUMBER: 33,208
XX REFERENCE/DOCKET NUMBER: 9001-0016.21
XX TELECOMMUNICATION INFORMATION:
XX TELEPHONE: (415) 617-8999
XX TELEFAX: (415) 327-3231
XX INFORMATION FOR SEQ ID NO: 6:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 926 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
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QY 301 ESYAERFKKLGVDNLLAEYQRTGTIDASVTAINALAAIAGGVSAAAAGSVIASPIA 360  
Db 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVVEKNHGNKYNFENGVDARYLANLQD 420  
QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVVEKNHGNKYNFENGVDARYLANLQD 420  
Db 421 NMKFLNLNKLKELQAEVIAITQQQDNNIGDLAGISRLGKVLGSKRAYVDAFEEGKHKA 480  
QY 421 NMKFLNLNKLKELQAEVIAITQQQDNNIGDLAGISRLGKVLGSKRAYVDAFEEGKHKA 480  
Db 481 DKLVLDSANGIIDVSNKAKTQHILFRTPLTPTGTEHRVQTKYETITKLNINRVD 540  
QY 481 DKLVLDSANGIIDVSNKAKTQHILFRTPLTPTGTEHRVQTKYETITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDAGISRLGKVLGSKRAYVDAFEEGKHKA 600  
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGISRLGKVLGSKRAYVDAFEEGKHKA 600  
Db 601 DKGEGYDRVHYSRGNKALIDATKETEEOGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
QY 601 DKGEGYDRVHYSRGNKALIDATKETEEOGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
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QY 661 KIEYRHSNNQHHAGYTTKDTLKAVEEIICTSHNDIFKGSKFNDAFNGDGVDTIDGNDGN 720  
Db 721 DRLFPGKGDDILDGGNGDDIFDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFPGKGDDILDGGNGDDIFDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
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Db 841 NGERITSQVDDLIAGKNGKITQDELKSVYDNYELLKHSKNVNSLDKLSSVSAFTSSN 900  
QY 841 NGERITSQVDDLIAGKNGKITQDELKSVYDNYELLKHSKNVNSLDKLSSVSAFTSSN 900  
Db 901 DSRNLVAPTSMLDQSLSSLOFARQS 926  
QY 901 DSRNLVAPTSMLDQSLSSLOFARQS 926

RESULT 8  
ID US-08-455-970A-2 STANDARD: PRT: 926 AA.

AC xxxxxx

Sequence 2, Application US/08455970A

Sequence 2, Application US/08455970A

Patent No. 5708155

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

TITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455,970A  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960,932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 926 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 926 AA: 99346 MW: 4207190 CN;

Query Match 98.6%; Score 6128; DB 1; Length 926;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 NMKFLNLNKLKELQAEVIAITQQQDNNIGDLAGISRLGKVLGSKRAYVDAFEEGKHKA 480  
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QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGISRLGKVLGSKRAYVDAFEEGKHKA 600  
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QY 661 KIEYRHSNNQHHAGYTTKDTLKAVEEIICTSHNDIFKGSKFNDAFNGDGVDTIDGNDGN 720

Db 721 DRLEGGKDDILDDGGDDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780  
QY 721 DRLEGGKDDILDDGGDDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780  
Db 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEEIIQ 840  
QY 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEEIIQ 840  
Db 841 NGERITSKQVDDLLAKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLSSVSFTSSN 900  
QY 841 NGERITSKQVDDLLAKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLSSVSFTSSN 900  
Db 901 DSRNVLVAPTSMLDQSLSSLOFARG 926  
QY 901 DSRNVLVAPTSMLDQSLSSLOFARG 926  
RESULT 9  
ID US-08-455-970A-10 STANDARD: PRT: 943 AA.  
XX  
AC xxxxxx  
XX  
DT  
XX  
XX  
DE  
XX  
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CC Sequence 10, Application US/08455970A  
CC Patent No. 5708155  
CC GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.  
CC APPLICANT: REDMOND, MARK J.  
CC APPLICANT: HUGHES, HUI P.A.  
CC  
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
CC  
CC NUMBER OF SEQUENCES: 15  
CC  
CC CORRESPONDENCE ADDRESS:  
CC  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455,970A  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960,932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 10:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 943 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 943 AA: 101229 MW: 4397993 CN:  
Query Match 98.6%; Score 6128; DB 1; Length 943;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEONGLQDLVKAEEELGIEVQREERNIATA 60  
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QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGQISQFGSKL 180  
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QY 361 LLVSGITGVISTILOYSKQAMFEHVANKHNKIVWEKNNHGNFYFENGVDARYLANLQD 420  
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QY 421 NKVELLNKELQAEVITATQOQWDDNIGDLAISRLGKVLGSKAYVDAFEKGHIKA 480  
Db 481 DKLVLQDSANGIIDVSNKRAKTOHILFRPLTPGTEHRRVOTKYEYITKLNINRVD 540  
QY 481 DKLVLQDSANGIIDVSNKRAKTOHILFRPLTPGTEHRRVOTKYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNVVQRIEIDNAGNVTKETKIIAKLGEEDDNNVFGSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNVVQRIEIDNAGNVTKETKIIAKLGEEDDNNVFGSGTTEI 600  
Db 601 DGGGYDRVHYSRGNYGALTIDATKETEQQSYTVNRVETGKALHEVTSTHTALVGNREE 660  
QY 601 DGGGYDRVHYSRGNYGALTIDATKETEQQSYTVNRVETGKALHEVTSTHTALVGNREE 660  
Db 661 KIEYRHSNNQHAGYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGDGVDTIDGNDGN 720  
QY 661 KIEYRHSNNQHAGYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGDGVDTIDGNDGN 720  
Db 721 DRLEGGKDDILDDGGDDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780  
QY 721 DRLEGGKDDILDDGGDDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780  
Db 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEEIIQ 840  
QY 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEEIIQ 840  
Db 841 NGERITSKQVDDLLAKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLSSVSFTSSN 900  
QY 841 NGERITSKQVDDLLAKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLSSVSFTSSN 900  
Db 901 DSRNVLVAPTSMLDQSLSSLOFARG 926  
QY 901 DSRNVLVAPTSMLDQSLSSLOFARG 926  
RESULT 10  
ID US-08-455-970A-14 STANDARD: PRT: 951 AA.  
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AC xxxxxx  
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DT  
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Sequence 14, Application US/08455970A  
 Sequence 14, Application US/08455970A  
 Patent No. 5708155  
 GENERAL INFORMATION:  
 APPLICANT: POTTER, ANDREW A.  
 APPLICANT: REDMOND, MARK J.  
 APPLICANT: HUGHES, HUW P.A.  
 TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
 TITLE OF INVENTION: CHIMERAS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: REED & ROBINS  
 STREET: 285 HAMILTON AVENUE, SUITE 200  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,970A  
 FILING DATE: 31-MAY-1995  
 CLASSIFICATION: 424  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/960,932  
 FILING DATE: 14-OCT-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 9001-0016.10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 327-3400  
 TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 951 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE 951 AA; 102128 MW; 4463354 CN;

Query Match 98.6%; Score 6128; DB 1; Length 951;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKGAKKILYIPQNYQYDTEOGNGLQDLVKAARELGIEVQREERNNTA 60  
 Qy 1 MATVIDLSFPKTKGAKKILYIPQNYQYDTEOGNGLQDLVKAARELGIEVQREERNNTA 60  
 Db 61 QTSLGTTQTALGLTERGIVLSPAQIDKLLQTKAGALGSAESIVQNAKAKTVLSGIQS 120  
 Qy 61 QTSLGTTQTALGLTERGIVLSPAQIDKLLQTKAGALGSAESIVQNAKAKTVLSGIQS 120  
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 Db 181 QNIRKGLTGLDKLNNIGGLDAGLGVISGLLSGATAALVLAADKNASTAKKVGAGFELA 240  
 Qy 181 QNIRKGLTGLDKLNNIGGLDAGLGVISGLLSGATAALVLAADKNASTAKKVGAGFELA 240  
 Db 241 NOVVGNTIKAVSSYLQORVAAGSSGTPVAALIASTVSLAISPLAFAGTADKFNHAKSL 300  
 Qy 241 NOVVGNTIKAVSSYLQORVAAGSSGTPVAALIASTVSLAISPLAFAGTADKFNHAKSL 300  
 Db 301 ESYAERFKKLGVDGNLLAEYQRTGTIDASVTAINALAAIAGVSAAGSVIAGSPIA 360  
 Qy 301 ESYAERFKKLGVDGNLLAEYQRTGTIDASVTAINALAAIAGVSAAGSVIAGSPIA 360

Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVWEKNNHKNYFENGVDARYLANLOD 420  
 Qy 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVWEKNNHKNYFENGVDARYLANLOD 420  
 Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGKVLGKAYVDAFEEGKHKA 480  
 Qy 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGKVLGKAYVDAFEEGKHKA 480  
 Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFTPLTPTGTEHRRVQTKYIITKLINRVD 540  
 Qy 481 DKLVQDLSANGIIDVNSGKAKTQHILFTPLTPTGTEHRRVQTKYIITKLINRVD 540  
 Db 541 SKKITDGAASSTFDLNNVQRIEIDNAGNVTKTETKIIAKLGGDDNVFVSGSTTEI 600  
 Qy 541 SKKITDGAASSTFDLNNVQRIEIDNAGNVTKTETKIIAKLGGDDNVFVSGSTTEI 600  
 Db 601 DGEGYDRVHYSRNGYALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNRE 660  
 Qy 601 DGEGYDRVHYSRNGYALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNRE 660  
 Db 661 KIEYRHSNNQHAGYTTKDTLKAVERIIIGTSHNDIPKSGKFNDAFNGGVDITDGNNGN 720  
 Qy 661 KIEYRHSNNQHAGYTTKDTLKAVERIIIGTSHNDIPKSGKFNDAFNGGVDITDGNNGN 720  
 Db 721 DRLFGGKGDDILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGDNDIITDSDGNDKLS 780  
 Qy 721 DRLFGGKGDDILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGDNDIITDSDGNDKLS 780  
 Db 781 FDSNLKDLTTFEKVKHNLVITNSKKEKVTIQNWFEADFAKEVPNKATKDEKIEIIGQ 840  
 Qy 781 FDSNLKDLTTFEKVKHNLVITNSKKEKVTIQNWFEADFAKEVPNKATKDEKIEIIGQ 840  
 Db 841 NGRITSQVDDLIAGKNGKITODELSKVVDNYELLKHKNTVNSLKLSSVSAFTSSN 900  
 Qy 841 NGRITSQVDDLIAGKNGKITODELSKVVDNYELLKHKNTVNSLKLSSVSAFTSSN 900  
 Db 901 DSRNLVAPTSMLDQSLSLQFARGS 926  
 Qy 901 DSRNLVAPTSMLDQSLSLQFARGS 926

RESULT 11  
 ID US-08-170-126-2 STANDARD; PRT: 1098 AA.  
 XX xxxxxx  
 XX  
 DT  
 XX  
 XX  
 DE Sequence 2, Application US/08170126  
 XX Sequence 2, Application US/08170126  
 CC Patent No. 5594107  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW  
 CC APPLICANT: CAMPOS, MANUEL  
 CC APPLICANT: HUGHES, HUW P.A.  
 CC TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES  
 CC TITLE OF INVENTION: THEREOF  
 CC NUMBER OF SEQUENCES: 6  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS  
 CC STREET: 635 BRYANT STREET  
 CC CITY: PALO ALTO  
 CC STATE: CALIFORNIA  
 CC COUNTRY: UNITED STATES OF AMERICA  
 CC ZIP: 94301  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent In Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/170,126  
 CC FILING DATE: 08/08/1998



CC FILING DATE: 20-DEC-1993  
CC CLASSIFICATION: 530  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/777,715  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/571,301  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9000-0013.21  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1098 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1098 AA: 118577 MW: 5903750 CN:  
SQ  
  
Query Match 97.4%; Score 6057; DB 1; Length 1098;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 183 KTGAKKIILYIPONYQYDTEQNGLDLVKAAEBELGIEVOREERNNIATAQSLGTIQT 242  
QY 11 KTGAKKIILYIPONYQYDTEQNGLDLVKAAEBELGIEVOREERNNIATAQSLGTIQT 70  
  
Db 243 IGLTERGIVLSAPOIDKLQTKAGALGSAESIVONANKAKTVLSGIOSILGSVLGMD 302  
QY 71 IGLTERGIVLSAPOIDKLQTKAGALGSAESIVONANKAKTVLSGIOSILGSVLGMD 130  
  
Db 303 LDEALQNNNOHAKAGLELTNSLIENIANSYKTLDEFGEQISQFGSKLQNIKGLGTIG 362  
QY 131 LDEALQNNNOHAKAGLELTNSLIENIANSYKTLDEFGEQISQFGSKLQNIKGLGTIG 190  
  
Db 363 DLKNTGGDLKAGLDVIGSLGSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 422  
QY 191 DLKNTGGDLKAGLDVIGSLGSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 250  
  
Db 423 VSSYILAQRVAAGLSGTGPAALIASTVSLATISPLAFAGIADKFNHAKSLEYAERFKL 482  
QY 251 VSSYILAQRVAAGLSGTGPAALIASTVSLATISPLAFAGIADKFNHAKSLEYAERFKL 310  
  
Db 483 GYDGNLLAEYQRTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIALLVSGITGYI 542  
QY 311 GYDGNLLAEYQRTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIALLVSGITGYI 370  
  
Db 543 STILOYSKQAMFEHVANKIHNKIVEKKNHKNYFENGYDARYLANLDNMKFLNLNK 502  
QY 371 STILOYSKQAMFEHVANKIHNKIVEKKNHKNYFENGYDARYLANLDNMKFLNLNK 430  
  
Db 603 ELQAEVIAITOOQDNNIGDLAGISRLGEKVLGSKAYVDAEEGKHIRADKLVLQDLSAN 662  
QY 431 ELQAEVIAITOOQDNNIGDLAGISRLGEKVLGSKAYVDAEEGKHIRADKLVLQDLSAN 490  
  
Db 663 GIIDVNSGKAKTHILFRPLTPTGTEHRRVQTKYEYITKLNINRVDSWKITDGAAS 722  
QY 491 GIIDVNSGKAKTHILFRPLTPTGTEHRRVQTKYEYITKLNINRVDSWKITDGAAS 550  
  
Db 723 STFDLTNVQVIGIELDNAGNVTKTETKIIAKLGGEDDNVFGSGTTTIDGEGYDRVH 782  
QY 551 STFDLTNVQVIGIELDNAGNVTKTETKIIAKLGGEDDNVFGSGTTTIDGEGYDRVH 610  
  
Db 783 YSRGNGALTIDATKETEQSYTVNFEVETGKALHEVTSHTHALVGNREEKTEYRHSNQ 842  
QY 611 YSRGNGALTIDATKETEQSYTVNFEVETGKALHEVTSHTHALVGNREEKTEYRHSNQ 670  
  
Db 843 HHAGYTKDTLKAVEEIICTSHNDIFKGSFNDAFNGGVDITDGNDRNLFGGKGD 902  
QY 671 HHAGYTKDTLKAVEEIICTSHNDIFKGSFNDAFNGGVDITDGNDRNLFGGKGD 730

Db 903 ILDGGNGDDFIDGGKGNLHGGKGDIDFVHRKGDGNDIITDSDGNDKLSFSDSNLKDLT 962  
QY 731 ILDGGNGDDFIDGGKGNLHGGKGDIDFVHRKGDGNDIITDSDGNDKLSFSDSNLKDLT 790  
  
Db 963 FEKVKNLVIITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQNGERITSQV 1022  
QY 791 FEKVKNLVIITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQNGERITSQV 850  
  
Db 1023 DDIAKNGKITQDLSKVVDNYELLKHKSNVTNSLKLISVSFTSSNDSRNVLVAPT 1082  
QY 851 DDIAKNGKITQDLSKVVDNYELLKHKSNVTNSLKLISVSFTSSNDSRNVLVAPT 910  
  
Db 1083 SMLDQSLSSLOFARGS 1098  
QY 911 SMLDQSLSSLOFARGS 926  
  
RESULT 12  
ID US-07-777-715-7 STANDARD; PRT; 1098 AA.  
XX  
AC xxxxxx  
XX  
DT  
XX  
DE  
XX  
Sequence 7, Application US/07777715  
Sequence 7, Application US/07777715  
Patent No. 5273889  
GENERAL INFORMATION:  
CC APPLICANT: Potter, Andrew  
CC APPLICANT: Campos, Manuel  
CC APPLICANT: Hughes, Huw P.A.  
CC TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND  
CC TITLE OF INVENTION: USES THEREOF  
CC NUMBER OF SEQUENCES: 9  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Morrison & Foerster  
CC STREET: 545 Middlefield Road, Suite 200  
CC CITY: Menlo Park  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94025  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/777,715  
CC FILING DATE: 19911016  
CC CLASSIFICATION: 424  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 29310-2001320  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-327-7250  
CC TELEFAX: 415-327-2951  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1098 amino acids  
CC TYPE: AMINO ACID  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1098 AA: 118577 MW: 5903750 CN;  
SQ  
  
Query Match 97.4%; Score 6057; DB 1; Length 1098;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 183 KTGAKKIILYIPONYQYDTEQNGLDLVKAAEBELGIEVOREERNNIATAQSLGTIQT 242

QY 11 KTGAKKIILYIPQNYDYTEQNGLODLVKAABEELGIEVQREERNNIATQAISLGTIQT 70  
Db 243 IGLTERGIVLSAPOIDKLLQKTKAGQALGSAESIVONANKAKTVLSGIGSLGVLGMD 302  
QY 71 IGLTERGIVLSAPOIDKLLQKTKAGQALGSAESIVONANKAKTVLSGIGSLGVLGMD 130  
Db 303 LDEALQNNNOHALAKAGLELNSLIENTANSVKTIDFEGEQISQFGSKLQNIKGLGTIG 362  
QY 131 LDEALQNNNOHALAKAGLELNSLIENTANSVKTIDFEGEQISQFGSKLQNIKGLGTIG 190  
Db 363 DKLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 422  
QY 191 DKLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 250  
Db 423 VSSYILAQVRAAGLSSTGTPVAALIASTVSLATSPAFAGIADKFNHAKSLESYAERFKL 482  
QY 251 VSSYILAQVRAAGLSSTGTPVAALIASTVSLATSPAFAGIADKFNHAKSLESYAERFKL 310  
Db 483 GYDGDNLAEYORGCTGTIDASVTANTALAAATAGGVSAAAGSVIASPALLVSGITGYI 542  
QY 311 GYDGDNLAEYORGCTGTIDASVTANTALAAATAGGVSAAAGSVIASPALLVSGITGYI 370  
Db 543 STILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGYDARYLANODNMKFLNLNK 602  
QY 371 STILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGYDARYLANODNMKFLNLNK 430  
Db 603 ELQAEVIAITOOOWDNNIGDLGASIRLGEKVLGSKAYVDAPEEGKHAKADKLVLQDSAN 662  
QY 431 ELQAEVIAITOOOWDNNIGDLGASIRLGEKVLGSKAYVDAPEEGKHAKADKLVLQDSAN 490  
Db 663 GIIDVNSGKAKTOHLFRTPLTPGTEHRRVOTQKYEYIKLNINRVDSWKITDGAAS 722  
QY 491 GIIDVNSGKAKTOHLFRTPLTPGTEHRRVOTQKYEYIKLNINRVDSWKITDGAAS 550  
Db 723 STFDLNVVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGTTEIDGEGYDRVH 782  
QY 551 STFDLNVVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGTTEIDGEGYDRVH 610  
Db 783 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 842  
QY 611 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 670  
Db 843 HHAGYVTKOTLKAVEELIIGTSHNDIFKSGFNDAFNGDGDVDTIDGNDGNRLFGKGDD 902  
QY 671 HHAGYVTKOTLKAVEELIIGTSHNDIFKSGFNDAFNGDGDVDTIDGNDGNRLFGKGDD 730  
Db 903 ILDGGNGDDFIDGGKNDLLHGGKGDDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDLT 962  
QY 731 ILDGGNGDDFIDGGKNDLLHGGKGDDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDLT 790  
Db 963 FEKVHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEEIIIGQNGERITSKV 1022  
QY 791 FEKVHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEEIIIGQNGERITSKV 850  
Db 1023 DDLIANGNKITODELSKVVDNYELLKHSKNVNSLDKLISVSATSSNDSNRVLVAPT 1082  
QY 851 DDLIANGNKITODELSKVVDNYELLKHSKNVNSLDKLISVSATSSNDSNRVLVAPT 910  
Db 1083 SMLDQSLSSLOFARGS 1098  
QY 911 SMLDQSLSSLOFARGS 926

RESULT 13  
ID US-08-215-805A-80 STANDARD; PRT; 934 AA.

XX AC xxxxxx

XX DT

XX DE

XX Sequence 80, Application US/08215805A

XX Sequence 80, Application US/08215805A

CC Patent No. 5559008  
CC GENERAL INFORMATION:  
CC APPLICANT: Chang, Yung-Fu  
CC TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURCELLA  
CC TITLE OF INVENTION: SUIS  
CC NUMBER OF SEQUENCES: 84  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
CC STREET: Clinton Square, P.O. Box 1051  
CC CITY: Rochester  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 14603  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA: US/08/215,805A  
CC APPLICATION NUMBER: US/08/215,805A  
CC FILING DATE: 22-MAR-1994  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Timian, Susan J.  
CC REGISTRATION NUMBER: 34,103  
CC REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (716) 263-1636  
CC TELEFAX: (716) 263-1600  
CC INFORMATION FOR SEQ ID NO: 80:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 934 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS:  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC ORIGINAL SOURCE:  
CC ORGANISM: Pasteurella suis  
CC STRAIN: 5943  
CC IMMEDIATE SOURCE:  
CC LIBRARY: P. suis DNA in Bacteriophage lambda-dash  
CC CLONE: (Lambda)7fc33-37  
CC SEQUENCE 934 AA; 100477 MW; 4245576 CN;

Query Match 79.2%; Score 4925; DB 1; Length 934;  
Best Local Similarity 79.8%; Pred. No. 0.00e+00;  
Matches 705; Conservative 112; Mismatches 66; Indels 1; Gaps 1;

Db 34 KAGAKKILYIPDYEDSGRNGIQLVKAEDLGIEVQREERNGIATAQNSLSTIQNI 93  
QY 11 KTGAKKIILYIPQNYDYTEQNGLODLVKAABEELGIEVQREERNNIATQAISLGTIQT 70  
Db 94 LGFSERGIVLSAPOIDKLLQKTKAGQALGSAESIVONANKAKTVLSGIGSLGVLGMD 153  
QY 71 IGLTERGIVLSAPOIDKLLQKTKAGQALGSAESIVONANKAKTVLSGIGSLGVLGMD 130  
Db 154 LDEILKNKSGELDLAKAGLELNSLIENTANSVOTLDFSEIQISQIGTKLQNVKGLGTIG 213  
QY 131 LDEALQNNNOHALAKAGLELNSLIENTANSVKTIDFEGEQISQFGSKLQNIKGLGTIG 190  
Db 214 DKLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 273  
QY 191 DKLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 250  
Db 274 VSSYILAQVRAAGLSSTGTPVAALIASTVSLATSPAFAGIADKFNHAKSLESYAERFKL 333  
QY 251 VSSYILAQVRAAGLSSTGTPVAALIASTVSLATSPAFAGIADKFNHAKSLESYAERFKL 310  
Db 334 GYDGDNLAEYORGCTGTIDASVTANTALAAATAGGVSAAAGSVIASPALLVSGITGYI 393  
QY 311 GYDGDNLAEYORGCTGTIDASVTANTALAAATAGGVSAAAGSVIASPALLVSGITGYI 370  
Db 394 STILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGYDARYLANODNMKFLNLNK 453

|||||  
QY 371 STILOYSQAMEEHVANKIHNKIVSEKNNHGNKYNFENGVDARYLANQDNKFLNKLK 430  
Db 454 ELQAEVIRITQOQNDNIGNLAGISRLGKVMKSKAYADAFEEGKLKADTFVOLDSAT 513  
QY 431 ELQAEVIRITQOQNDNIGNLAGISRLGKVMKSKAYADAFEEGKLKADTFVOLDSAT 490  
Db 514 GVINTSKSDNVKTHILFRTPLLTGTVENRRRIQGVKYEYITKLNINRVDSWKKITDGN 573  
QY 491 GIIDVSNKGAKTQHILFRTPLLTGTEHREVRVQGVKYEYITKLNINRVDSWKKITDGN 550  
Db 574 STFDLTNNVQVIGIELDHADNVKTKETKIITANLGDGNDVFIQSGTTEVDGNGDLRVH 633  
QY 551 STFDLTNNVQVIGIELDHADNVKTKETKIITANLGDGNDVFIQSGTTEVDGNGDLRVH 610  
Db 634 YSRGDYGALTIDATNESVQGSYTVKRFVETGKALHEVTVATQSVLVGSREEKIEYRHSNNT 693  
QY 611 YSRGNYGALTIDATNESVQGSYTVKRFVETGKALHEVTVATQSVLVGSREEKIEYRHSNNT 670  
Db 694 QHAGYTTDTLKSVEEIIIGTSRNDIFKSKFDDAFHGGDGVNDIDGNAGNDRLFGGKGF 753  
QY 671 HHAGYTTDTLKSVEEIIIGTSRNDIFKSKFDDAFHGGDGVNDIDGNAGNDRLFGGKGF 730  
Db 754 IIDGGDGDFFIDGGDGDILHGGKNDILCTVKG-GNDSISDGGNDRLSPADSNLKDLT 812  
QY 731 ILDGGDGDFFIDGGKNDLHGGKNDILCTVKG-GNDSISDGGNDRLSPADSNLKDLT 790  
Db 813 FEKVNHMLTNNVKEKVTYQNWFEADYKTVHNYQATADKIEEIIIGROGERITSKQI 872  
QY 791 FEKVHMLTNNVKEKVTYQNWFEADYKTVHNYQATADKIEEIIIGROGERITSKQI 850  
Db 873 DELIEKGGKIDQSELERIASSALLKSKFASNSLNKLVSAA 916  
QY 851 DDLIAGKNGKITQDLSKVDVNDYELKSKNVTNSLDKLISVS 894

## RESULT 14

ID .PCT-US93-10500-2 STANDARD: PRT: 1244 AA.  
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AC xxxxxx  
XX  
DT  
DE  
XX  
Sequence 2, Application PC/TUS9310500  
CC  
CC GENERAL INFORMATION:  
CC APPLICANT: Chang, Yung-Fu  
CC TITLE OF INVENTION: Recombinant Vaccine For Procine  
CC TITLE OF INVENTION: Pleuropneumoniae  
CC NUMBER OF SEQUENCES: 2  
CC CORRESPONDENCE ADDRESS:  
CC STREET: 1600 Empire Tower  
CC CITY: Buffalo  
CC STATE: New York  
CC COUNTRY: U.S.A.  
CC ZIP: 14202  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/10500  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/972,229  
CC FILING DATE: 05-NOV-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Korman, Alan S.  
CC REGISTRATION NUMBER: 33,932

REFERENCE/DOCKET NUMBER: 19603/00001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-853-8104  
TELEFAX: 716-853-8109  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1244 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Actinobacillus pleuropneumoniae  
STRAIN: Serotypes 2, 3, 4, 6 and 8  
INDIVIDUAL ISOLATE: Swine  
CELL TYPE: Gram negative bacterium  
SQ SEQUENCE 1244 AA; 135397 MW; 7631235 CN;  
Query Match 41.3%; Score 2566; DB 2; Length 1244;  
Best Local Similarity 52.2%; Pred. No. 6.12e-178;  
Matches 401; Conservative 177; Mismatches 167; Indels 23; Gaps 20;  
Db 228 GNKLVVIP-K-EYDGSVGVGFFDLVKAABELGIQVYVNRNEVAHSLGTADQPLGL 285  
QY 14 AKRIILYIPONYQYDEQGNLQDLVKAABELGIEVQREERNIATQTSILGTIQTAL 73  
Db 286 TERGLTFAFOLQFLOKHSKISNVVGSSTGDAVSKLAKSQTIIISGIVSLVGLAGINL 345  
QY 74 TERGIVLSAPQIDKLLQK-TRAGOALGSABES-IVONANKARTVLGSIQSLVGLAGMDL 131  
Db 346 NEAIIISGSELELAEGVSLASELVNSIAKGTITIDAFITQIONFG-KLAENAKGLGVG 404  
QY 132 DEALQNNNQHALAKAGLELTNSLIENIANSVKLTDFEGEIQISQFGSKL-QNIKGLGLT 190  
Db 405 RQONISGSALSKTGLDIIISLLSGVTSRFPALRNKNASTSTKVAAGFELSNOVIGIT 464  
QY 191 DKLKNIIG--LDRKAGLDVIGSLGATAALVLADKNASTAKKVGAGFELANQVGVNIT 248  
Db 465 KAVSSYILAORLRLAGLSTTGPAAALTAASSISLAISPLAFLRVADNFRSKEIGEFARFK 524  
QY 249 KAVSSYILAORVAAGLSTGTPVAALTAISTVSLAISPLAFAGIADKFNHAKSLSEYARFK 308  
Db 525 KLGVDGDKLSEFYHEAGTIDASTITISTALSAITAGTAASAGALVGPITLLVTGITG 584  
QY 309 KLGVDGDNLLAEYQRCGTIDASTVTAINTALAAAGVSAAGSVIASPALLVSGITG 368  
Db 585 LISGILEFSKQPMLDHVASKIGNKIDWEKK-YGKNYFENGVDARHKAFLFEDSFLSSSF 643  
QY 369 VISTILOYSQAMFEHVANKIHNKIVSEKNNHGNKYNFENGVDARYLANQDNKFLNKL 428  
Db 644 NKQYETERAVLITQORWDEYIGELAGITGKDKLSSGKAYVDYFQEGKLEKPPDFSKV 703  
QY 429 NKLQAEVIRITQOQNDNIGNLAGISRLGKVMKSKAYADAFEEGKLKADTFVOLD 484  
Db 704 VFDPKGEIDISNS-QTSTL-LKFVTPLLTPGTESRETRTQTKYEYITKLVKWKGVKVV 761  
QY 485 QLODSANGIIDVSNKGAKTQHILFRTPLLTGTEHREVRVQGVKYEYITKLNINRVDSW 544  
Db 762 NGVKDKAVYDYNLQIAHIS-SSVARGEEYREVLVSHLGNNGNDKVFLLAAGSAEIHAG 820  
QY 545 TDGAA-SSTFDLTNNVQVIGIELDHADNVKTKETKIITANLGDGNDVFIQSGTTE 603  
Db 821 EGHVYVYDQTDGLVLDGCTKATEOGRYSVTRELSCATKILREVINKQYKAVKRETEL 880  
QY 604 EGDVRVHSRGNTGALTIDATKETEQQSYTVNR-FVETGKALHEVTVATQSVLVGSREEK 662  
Db 881 EYRDYELTQSGNSNLKAHDLHLSVEET-GSNQRDEKFSKFRDIFHGADGDDLLNGDNG 939  
QY 663 EYRHSN-NQH-HAGYITKDTLKAVEEIIIGTSRNDIFKSKFDDAFHGGDGVNDIDGN 720

Db 940 DILYDKNDELRCNGNDOLYGGEGDDKLLGGNGNN-YL-SGGDGN 985  
Qy 721 DRLEGGKDDILDCGNGDDFIDGGKNDLLHGGKGDIFVHRKGDND 768

RESULT 15  
ID US-08-387-156-10 STANDARD; PRT; 544 AA.  
XX XXXXX

Sequence 10, Application US/08387156  
Sequence 10, Application US/08387156  
Patent No. 5723129  
GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.  
CC APPLICANT: REDMOND, MARK J.  
CC APPLICANT: HUGHES, HUW P.A.  
CC TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS  
CC NUMBER OF SEQUENCES: 28  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 635 BRYANT STREET  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,156  
FILING DATE: 10-FEB-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,932  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,171  
FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 9001-0016.21

TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 544 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE 544 AA: 57542 MW; 1502532 CN;

Query Match 36.0%; Score 2239; DB 1: Length 544;  
Best Local Similarity 100.0%; Pred. No. 1.35e-153;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKGAKIILYIPONYQYDTEOGLQDLVKAEEELGIEVQREERNIATA 60  
Qy 1 MATVIDLSFPKTKGAKIILYIPONYQYDTEOGLQDLVKAEEELGIEVQREERNIATA 60  
Db 61 QTSGLTIQTATGLTGERIVLSAPQIDKLLQTKAGQALGSAESIVQNANKAKTVLSGIQS 120  
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Db 121 ILGSVLGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180

Qy 121 ILGSVLGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180  
Db 181 QNTKGLGTGLGDKLKNIGGLDKAGLDVIGSGLLSGATAALVLADKNASTAKKVGAGFELA 240  
Qy 181 QNTKGLGTGLGDKLKNIGGLDKAGLDVIGSGLLSGATAALVLADKNASTAKKVGAGFELA 240  
Db 241 NOVVGNTTKAVSSYIIAORVAAGLSSTGPVAAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
Qy 241 NOVVGNTTKAVSSYIIAORVAAGLSSTGPVAAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
Db 301 ESYAERFKILGYDGNLLAEYQRTGTIDASVTAINATAAIAAGGVSAAAA 351  
Qy 301 ESYAERFKILGYDGNLLAEYQRTGTIDASVTAINATAAIAAGGVSAAAA 351

Search completed: Wed Dec 9 19:31:17 1998  
Job time : 55 secs.



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WQESREH  
(TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MFSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:31:35 1998; MasPar time 45.64 Seconds

Tabular output not generated. 770.326 Million cell updates/sec

Title: >US-08-455-970-12  
Description: (1-936) from US08455970.pep  
Perfect Score: 6217  
Sequence: 1 MATVIDLSFPTGAKKILY.....LSSLFARGSQHWSYGLRPG 936

Scoring table: PAM 150  
Gap 11

Searched: 318656 seqs, 37563770 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-pending  
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85  
10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP  
17:NEWU8 18:NEWU9

Statistics: Mean 38.748; Variance 234.154; scale 0.165

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6217	100.0	936	US-08-455-	Sequence 12, Applicati	0.00e+00
2	6217	100.0	936	US-07-779-	Sequence 10, Applicati	0.00e+00
3	6217	100.0	977	US-08-124-	Sequence 8, Applicati	0.00e+00
4	6217	100.0	977	US-08-634-	Sequence 8, Applicati	0.00e+00
5	6217	100.0	977	US-08-878-	Sequence 8, Applicati	0.00e+00
6	6128	98.6	926	US-08-535-	Sequence 2, Applicati	0.00e+00
7	6128	98.6	926	US-08-694-	Sequence 6, Applicati	0.00e+00
8	6128	98.6	926	US-08-455-	Sequence 2, Applicati	0.00e+00
9	6128	98.6	926	US-08-878-	Sequence 6, Applicati	0.00e+00
10	6128	98.6	926	US-07-779-	Sequence 14, Applicati	0.00e+00
11	6128	98.6	926	US-09-124-	Sequence 6, Applicati	0.00e+00
12	6128	98.6	943	US-08-455-	Sequence 10, Applicati	0.00e+00
13	6128	98.6	943	US-07-779-	Sequence 12, Applicati	0.00e+00
14	6128	98.6	951	US-07-779-	Sequence 8, Applicati	0.00e+00
15	6128	98.6	951	US-08-455-	Sequence 14, Applicati	0.00e+00
16	6117	98.4	924	US-08-619-	Sequence 8, Applicati	0.00e+00
17	6117	98.4	924	US-08-038-	Sequence 8, Applicati	0.00e+00
18	6117	98.4	924	US-08-038-	Sequence 12, Applicati	0.00e+00
19	6117	98.4	924	US-08-038-	Sequence 15, Applicati	0.00e+00
20	4925	79.2	1111	US-07-972-	Sequence 2, Applicati	0.00e+00
21	4925	79.2	1111	US-07-972-	Sequence 2, Applicati	0.00e+00

22 4925 79.2 1111 3 US-07-972-Sequence 2, Applicatio 0.00e+00  
23 4254 68.4 956 7 US-08-396-Sequence 8, Applicatio 6.27e-288  
24 2566 41.3 1049 7 US-08-396-Sequence 11, Applicati 8.40e-168  
25 2566 41.3 1244 4 US-08-072-Sequence 2, Applicatio 2.64e-148  
26 2291 36.9 1022 7 US-08-396-Sequence 10, Applicati 1.27e-144  
27 2239 36.0 544 15 US-09-124-Sequence 10, Applicati 1.27e-144  
28 2239 36.0 544 10 US-08-694-Sequence 10, Applicati 1.27e-144  
29 2239 36.0 544 12 US-08-878-Sequence 10, Applicati 1.27e-144  
30 2194 35.3 699 15 US-09-124-Sequence 16, Applicati 1.96e-141  
31 2194 35.3 699 10 US-08-694-Sequence 16, Applicati 1.96e-141  
32 2167 34.9 1403 10 US-08-694-Sequence 17, Applicati 1.60e-139  
33 2167 34.9 1403 9 US-08-535-Sequence 3, Applicatio 1.60e-139  
34 2167 34.9 1403 15 US-09-124-Sequence 2, Applicatio 3.02e-50  
35 896 14.4 1706 10 US-08-669-Sequence 4, Applicatio 1.27e-49  
36 887 14.3 1705 10 US-08-669-Sequence 3, Applicatio 7.29e-13  
37 345 5.5 693 3 US-07-972-Sequence 3, Applicatio 7.29e-13  
38 345 5.5 693 3 US-08-323-Sequence 2, Applicatio 1.01e-07  
39 265 4.3 1115 7 US-07-895-Sequence 2, Applicatio 1.01e-07  
40 265 4.3 1115 3 US-09-057-Sequence 4, Applicatio 7.57e-08  
41 267 4.3 1857 14 US-09-057-Sequence 2, Applicatio 8.76e-08  
42 266 4.3 1805 14 US-09-057-Sequence 7, Applicatio 8.76e-08  
43 266 4.3 997 7 US-08-387-Sequence 4, Applicatio 4.26e-05  
44 223 3.6 997 7 US-08-387-Sequence 4, Applicatio 4.26e-05  
45 223 3.6 997 7 US-08-387-Sequence 4, Applicatio 4.26e-05

## ALIGNMENTS

RESULT 1  
ID US-08-455-970-12 STANDARD; PRT; 936 AA.

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Sequence 12, Application US/08455970

Sequence 12, Application US/08455970

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P. A.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

TITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3400

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

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CC LENGTH: 936 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 936 AA; 100529 MW; 4311495 CN;

Query Match 100.0%; Score 6217; DB 8; Length 936;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKGAKKIIILYIPQNYQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
QY 1 MATVIDLSFPKTKGAKKIIILYIPQNYQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
Db 61 QTSLGTTQTALGTERGIVLSAPOIDKLLQKTAKAGALGSAESIVONANKAKTVLSGIQS 120
QY 61 QTSLGTTQTALGTERGIVLSAPOIDKLLQKTAKAGALGSAESIVONANKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGQISQFGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGQISQFGSKL 180
Db 181 QNKGGLTGLDKKNIGGLDKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNKGGLTGLDKKNIGGLDKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVGNITKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVGNITKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 ESYAERFKKLGDDGNLLAEAYRGTTGTDASVTANTALAAAGGVSAAAGSVTIASPIA 360
QY 301 ESYAERFKKLGDDGNLLAEAYRGTTGTDASVTANTALAAAGGVSAAAGSVTIASPIA 360
Db 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNVKWEKNNHKNFYFENGVDARYLANLQD 420
QY 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNVKWEKNNHKNFYFENGVDARYLANLQD 420
Db 421 NMKFLNLLNKLQAEVIAITQQQDNNIGDLAGISRLGEKVLGSKAYVDAFECKHIKA 480
QY 421 NMKFLNLLNKLQAEVIAITQQQDNNIGDLAGISRLGEKVLGSKAYVDAFECKHIKA 480
Db 481 DKLVLDSANGIIDVNSGKAKTQHILFRTPLLTGTEHRRVQTKYEYITKLNINRVD 540
QY 481 DKLVLDSANGIIDVNSGKAKTQHILFRTPLLTGTEHRRVQTKYEYITKLNINRVD 540
Db 541 SKKITDGAASSTFDLTNNVVRIGIELDNAGNVTKTKETIAKLGEGDDNVFVSGTTEI 600
QY 541 SKKITDGAASSTFDLTNNVVRIGIELDNAGNVTKTKETIAKLGEGDDNVFVSGTTEI 600
Db 601 DGGEGYDRVHSRGNYGALTIDATKETEQGSYTVNRVETGKALHEVTSHTALVGNREE 660
QY 601 DGGEGYDRVHSRGNYGALTIDATKETEQGSYTVNRVETGKALHEVTSHTALVGNREE 660
Db 661 KLEYRSHNNQHAGYTTKDTLKAVEEIIIGTSHNDIFKSKFNDAENGDDVTDICNDGN 720
QY 661 KLEYRSHNNQHAGYTTKDTLKAVEEIIIGTSHNDIFKSKFNDAENGDDVTDICNDGN 720
Db 721 DRLFCKGDDILDDGNGDDFIDGGKGNLLHGGKGGDIFVHRKGGNDIITDSGNDKLS 780
QY 721 DRLFCKGDDILDDGNGDDFIDGGKGNLLHGGKGGDIFVHRKGGNDIITDSGNDKLS 780
Db 781 FSDSNKDLTFEKKVKNLVIITNSKKEKVTIQNWFRPADFAKEVPNYKATKDEKIEIIGQ 840
QY 781 FSDSNKDLTFEKKVKNLVIITNSKKEKVTIQNWFRPADFAKEVPNYKATKDEKIEIIGQ 840
Db 841 NGERITTSQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900
QY 841 NGERITTSQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900
Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936
QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936
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RESULT 2
ID US-07-779-171-10 STANDARD; PRT; 936 AA.
XX
AC
XX
DT
XX
DE
XX
CC Sequence 10, Application US/07779171
CC GENERAL INFORMATION:
CC APPLICANT: Potter, Andrew A.
CC APPLICANT: Redmond, Mark J.
CC APPLICANT: Hughes, Huw P.A.
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
CC TITLE OF INVENTION: PASTEURELLA HEAMOLYTICA LEUKOTOXIN CHIMERAS
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morrison & Foerster
CC STREET: 545 Middlefield Road, Suite 200
CC CITY: Menlo Park
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94025
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/779,171
CC FILING DATE: 19911016
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 29310-2001600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-327-7250
CC TELEFAX: 415-327-2951
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 936 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 936 AA; 100529 MW; 4311495 CN;

Query Match 100.0%; Score 6217; DB 3; Length 936;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKGAKKIIILYIPQNYQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
QY 1 MATVIDLSFPKTKGAKKIIILYIPQNYQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
Db 61 QTSLGTTQTALGTERGIVLSAPOIDKLLQKTAKAGALGSAESIVONANKAKTVLSGIQS 120
QY 61 QTSLGTTQTALGTERGIVLSAPOIDKLLQKTAKAGALGSAESIVONANKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGQISQFGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGQISQFGSKL 180
Db 181 QNKGGLTGLDKKNIGGLDKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNKGGLTGLDKKNIGGLDKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVGNITKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVGNITKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
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QY 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNNVFGSGTTEI 600  
 Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQQSGTYVNRVETGKALHEVTSHTALVGNREE 660  
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQQSGTYVNRVETGKALHEVTSHTALVGNREE 660  
 Db 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720  
 QY 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720  
 Db 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780  
 QY 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780  
 Db 781 FDSNLKDLTFEKVKNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
 QY 781 FDSNLKDLTFEKVKNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
 Db 841 NGERITTSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 QY 841 NGERITTSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936  
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936

RESULT 4

ID US-08-694-865-8 STANDARD; PRG: 977 AA.  
 XX  
 AC xxxxxx

Sequence 8, Application US/08694865

Sequence 8, Application US/08694865  
 GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: MANN, JOHN G.  
 CC TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS  
 CC NUMBER OF SEQUENCES: 34  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS LLP  
 CC STREET: 285 HAMILTON AVENUE, SUITE 200  
 CC CITY: PALO ALTO  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 94301  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent in Release #1.0, Version #1.30  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/694,865  
 CC FILING DATE: 09-AUG-1996  
 CC CLASSIFICATION: 424  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: MCCracken, THOMAS P.  
 CC REGISTRATION NUMBER: 38,548  
 CC REFERENCE/DOCKET NUMBER: 9001-0016.22  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415)327-3400  
 CC TELEFAX: (415)327-3231  
 CC INFORMATION FOR SEQ ID NO: 8:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 977 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 977 AA: 104869 MW: 4761174 CN;

Query Match 100.0%; Score 6217; DB 10; Length 977;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MATVIDLSFPFGTGAKKIILYIPQNYQYDEQNGQLDLVKAEEELGIEVQREERNIATA 60  
 QY 1 MATVIDLSFPFGTGAKKIILYIPQNYQYDEQNGQLDLVKAEEELGIEVQREERNIATA 60  
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 Db 181 QNIKGLGTGLGKLNIGGLDRKAGLGLDVISGLLSGATLALVADKNASTAKKVGAGFELA 240  
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 QY 301 ESYAERFKLGYDGNLLAEYQRTGTIDASVTANTALAAIAGGVSAAAGSVIASPIA 360  
 Db 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGYDARYLANLQD 420  
 QY 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGYDARYLANLQD 420  
 Db 421 NMKFLNLNKLQAEVIAITQQQWMDNIGLAGISRLGKVLGSKAYVDAFEKGHIKA 480  
 QY 421 NMKFLNLNKLQAEVIAITQQQWMDNIGLAGISRLGKVLGSKAYVDAFEKGHIKA 480  
 Db 481 DKLVLDSANGIIDVSNKAKTOHILFRTPLTPTGTEHREVOYKVEYITKLNINRVD 540  
 QY 481 DKLVLDSANGIIDVSNKAKTOHILFRTPLTPTGTEHREVOYKVEYITKLNINRVD 540  
 Db 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNNVFGSGTTEI 600  
 QY 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNNVFGSGTTEI 600  
 Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQQSGTYVNRVETGKALHEVTSHTALVGNREE 660  
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQQSGTYVNRVETGKALHEVTSHTALVGNREE 660  
 Db 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720  
 QY 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720  
 Db 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780  
 QY 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780  
 Db 781 FDSNLKDLTFEKVKNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
 QY 781 FDSNLKDLTFEKVKNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840  
 Db 841 NGERITTSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 QY 841 NGERITTSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936  
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936

RESULT 5  
 ID US-08-878-748-8 STANDARD; PRG: 977 AA.  
 XX  
 AC xxxxxx





QY 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120  
Db 121 ILGSLVAGMDLDEALQNNQNHAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180  
QY 121 ILGSLVAGMDLDEALQNNQNHAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180  
Db 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240  
QY 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240  
Db 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
QY 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360  
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360  
Db 361 LLYVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNHKNYFENGVDARYLANLOD 420  
QY 361 LLYVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNHKNYFENGVDARYLANLOD 420  
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGRHKA 480  
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGRHKA 480  
Db 481 DKLVQDSANGIIDVNSGKAKTQHILFRPTPLTPTGTEHRRVQTKYEVITKLNINRVD 540  
QY 481 DKLVQDSANGIIDVNSGKAKTQHILFRPTPLTPTGTEHRRVQTKYEVITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLNVVORIGIEDLNAGNVTKTKETKIIAKLGECDNVFVSGTTEI 600  
QY 541 SWKITDGAASSTFDLNVVORIGIEDLNAGNVTKTKETKIIAKLGECDNVFVSGTTEI 600  
Db 601 DGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRSHNNOHAGYTKDTLKAVEELIGTSHNDIFKGSKFNDFAFGDGVDTIDGNDGN 720  
QY 661 KIEYRSHNNOHAGYTKDTLKAVEELIGTSHNDIFKGSKFNDFAFGDGVDTIDGNDGN 720  
Db 721 DRLFPGKGDDILDGNGDDDFIDGKGNDLHGGKGGDDIFVHRKGDGNDIITDSGNDKLS 780  
QY 721 DRLFPGKGDDILDGNGDDDFIDGKGNDLHGGKGGDDIFVHRKGDGNDIITDSGNDKLS 780  
Db 781 FSDSNLKDLTFFERVKHNLVITNSKKEKVTIQNNWFREADFAKEVPNYKATKDEKIEELIG 840  
QY 781 FSDSNLKDLTFFERVKHNLVITNSKKEKVTIQNNWFREADFAKEVPNYKATKDEKIEELIG 840  
Db 841 NGERITSQVDDLIAGKNGKITODELSKVYDNYVELLKHKNVNSLDKLISSVSFTSSN 900  
QY 841 NGERITSQVDDLIAGKNGKITODELSKVYDNYVELLKHKNVNSLDKLISSVSFTSSN 900  
Db 901 DSRNLVAPTSMLDQSLSSLOFARGS 926  
QY 901 DSRNLVAPTSMLDQSLSSLOFARGS 926

RESULT 8  
ID US-08-455-970-2 STANDARD: PRT: 926 AA.

XX  
AC  
XX  
XX  
DT

Sequence 2, Application US/08455970  
Sequence 2, Application US/08455970  
GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.  
CC APPLICANT: REMOND, MARK J.  
CC APPLICANT: HUGHES, HUW P.A.

CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
CC TITLE OF INVENTION: CHIMERAS  
CC NUMBER OF SEQUENCES: 15  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455.970  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960.932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 926 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 926 AA; 99346 MW; 4207190 CN;

Query Match 98.6%; Score 6128; DB 8; Length 926;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPKTKGAKKILYIPONTYDTEQGNGLDVLKAAAEELGIEVQREERNIATA 60  
QY 1 MATVIDLSPKTKGAKKILYIPONTYDTEQGNGLDVLKAAAEELGIEVQREERNIATA 60  
Db 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120  
QY 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120  
Db 121 ILGSLVAGMDLDEALQNNQNHAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180  
QY 121 ILGSLVAGMDLDEALQNNQNHAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180  
Db 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240  
QY 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240  
Db 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
QY 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360  
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360  
Db 361 LLYVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNHKNYFENGVDARYLANLOD 420  
QY 361 LLYVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNHKNYFENGVDARYLANLOD 420  
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGRHKA 480  
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKAYVDFAFEGRHKA 480

Db 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLLTPTGTEHRRVQTKYEYITKLNINRVD 540  
QY 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLLTPTGTEHRRVQTKYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDNDAGNVTKTETKIIAKLGEEDDNNFVSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDNDAGNVTKTETKIIAKLGEEDDNNFVSGTTEI 600  
Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNNQHHAGYVTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIDGNDGN 720  
QY 661 KIEYRHSNNQHHAGYVTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIDGNDGN 720  
Db 721 DRLFGGKGGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFGGKGGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
Db 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIIQ 840  
QY 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIIQ 840  
Db 841 NGERITTSKOVDDLIAGNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900  
QY 841 NGERITTSKOVDDLIAGNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900  
Db 901 DSRNVLVAPTSMLDQSLSSLOFARGS 926  
QY 901 DSRNVLVAPTSMLDQSLSSLOFARGS 926

RESULT 9  
ID US-08-878-748-6 STANDARD; PRF: 926 AA.  
XX  
AC  
XX  
DT  
XX

Sequence 6, Application US/08878748

Sequence 6, Application US/08878748

GENERAL INFORMATION:  
APPLICANT: POTTER, ANDREW A.  
APPLICANT: REDMOND, MARK J.  
APPLICANT: HUGHES, HUW P.A.  
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REED & ROBINS  
STREET: 635 BRYANT STREET  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/878,748  
FILING DATE: 19-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,156  
FILING DATE: 10-FEB-1995  
APPLICATION NUMBER: US 07/960,932  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,171  
FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 9001-0016.21  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 926 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE 926 AA; 99346 MW; 4207190 CN;  
Query Match 98.6%; Score 6128; DB 12; Length 926;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDTEQNGLDLVKAAEELGIEVQREERNIIATA 60  
QY 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDTEQNGLDLVKAAEELGIEVQREERNIIATA 60  
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QY 61 QTSLGITQTAIGLTERGIVLSAPOIDKLLQKTAKAGALSAESIVONANKAKTVLSGIQS 120  
Db 121 ILGSVLACMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180  
QY 121 ILGSVLACMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180  
Db 181 QNIKGLGTGLDKLNIGGLDRAGLGVISGLSGATAALVADKNASTAKKVGAGFELA 240  
QY 181 QNIKGLGTGLDKLNIGGLDRAGLGVISGLSGATAALVADKNASTAKKVGAGFELA 240  
Db 241 NOVGNITKAVSSYILAORVAAGLSSTGPVAALTAISTVSLAISPLAFAGIADKNHAKSL 300  
QY 241 NOVGNITKAVSSYILAORVAAGLSSTGPVAALTAISTVSLAISPLAFAGIADKNHAKSL 300  
Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINALAAIAGGSVAAAAGSVIASPIA 360  
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINALAAIAGGSVAAAAGSVIASPIA 360  
Db 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIWEKNNHGNKYNFENGYDARYLANQD 420  
QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIWEKNNHGNKYNFENGYDARYLANQD 420  
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLGSLRGEKVLGSKAVYDAPFEGKHKA 480  
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLGSLRGEKVLGSKAVYDAPFEGKHKA 480  
Db 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLLTPTGTEHRRVQTKYEYITKLNINRVD 540  
QY 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLLTPTGTEHRRVQTKYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDNDAGNVTKTETKIIAKLGEEDDNNFVSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDNDAGNVTKTETKIIAKLGEEDDNNFVSGTTEI 600  
Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNNQHHAGYVTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIDGNDGN 720  
QY 661 KIEYRHSNNQHHAGYVTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDVTDIDGNDGN 720  
Db 721 DRLFGGKGGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFGGKGGDDILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
Db 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIIQ 840  
QY 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIIQ 840

QY 781 FSDSNLKDLEFVKVHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIQG 840  
 DB 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYVELLKHKNVTNSLDKLSSVSFTSSN 900  
 QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYVELLKHKNVTNSLDKLSSVSFTSSN 900  
 DB 901 DSRNLVAPTSMLDQSLSSLOFARG 926  
 QY 901 DSRNLVAPTSMLDQSLSSLOFARG 926  
 RESULT 10  
 ID US-07-779-171-14 STANDARD; PRT: 926 AA.  
 AC xxxxxx  
 DT  
 XX  
 XX  
 XX  
 XX  
 DE Sequence 14, Application US/07779171  
 CC Sequence 14, Application US/07779171  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Potter, Andrew A.  
 CC APPLICANT: Redmond, Mark J.  
 CC APPLICANT: Hughes, Huw P. A.  
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING  
 CC TITLE OF INVENTION: PASTEURELLA HEAMOLYTICA LEUKOTOXIN CHIMERAS  
 CC NUMBER OF SEQUENCES: 14  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Morrison & Foerster  
 CC STREET: 545 Middlefield Road, Suite 200  
 CC CITY: Menlo Park  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94025  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent in Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/07/779,171  
 CC FILING DATE: 19911016  
 CC CLASSIFICATION: 424  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Robins, Roberta L.  
 CC REGISTRATION NUMBER: 33,208  
 CC REFERENCE/DOCKET NUMBER: 29310-2001600  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415-327-7250  
 CC TELEFAX: 415-327-2951  
 CC TELEX: 706141  
 CC INFORMATION FOR SEQ ID NO: 14:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 926 amino acids  
 CC TYPE: AMINO ACID  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 926 AA; 99346 MW; 4207190 CN;  
 SQ  
 Query Match 98.68; Score 6128; DB 3; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 MATVIDLSFPKTKAKKILYIPONYQYDTQGNGLQDLVKAABEELGIEVOREERNIATA 60  
 QY 1 MATVIDLSFPKTKAKKILYIPONYQYDTQGNGLQDLVKAABEELGIEVOREERNIATA 60  
 DB 61 QTSGLGTQTAIGTERGIVLSAPQIDKLLQKTRAGQALGSAESIVQNAKAKTVLSGIQS 120  
 QY 61 QTSGLGTQTAIGTERGIVLSAPQIDKLLQKTRAGQALGSAESIVQNAKAKTVLSGIQS 120  
 DB 121 ILGSVLAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEFGQISQFGSKL 180

QY 121 ILGSVLAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEFGQISQFGSKL 180  
 DB 181 QNKGIGTIGDGLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240  
 QY 181 QNKGIGTIGDGLKNTGGDLKAGLDVTSGLSGATAALVLADKNASTAKKVGAGFELA 240  
 DB 241 NOVVGNTKAVSSYILAORVAAGLSTGPAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
 QY 241 NOVVGNTKAVSSYILAORVAAGLSTGPAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
 DB 301 ESYAERFKKLYGDDNLLAEYQRTGTIDASVTAINATAAGGVSAAAAGSVIASPTA 360  
 QY 301 ESYAERFKKLYGDDNLLAEYQRTGTIDASVTAINATAAGGVSAAAAGSVIASPTA 360  
 DB 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGVDARYLANLOD 420  
 QY 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGVDARYLANLOD 420  
 DB 421 NMKFLNLNKLQAEKVIAITQQQDNNIGDLAGISRLGKVLGSKAYVDAFEEGHKA 480  
 QY 421 NMKFLNLNKLQAEKVIAITQQQDNNIGDLAGISRLGKVLGSKAYVDAFEEGHKA 480  
 DB 481 DKLVLQDSANGIDVNSGKAKTQHILFRTPLTPTGTEHRERVOTGKYEYITKLNINRVD 540  
 QY 481 DKLVLQDSANGIDVNSGKAKTQHILFRTPLTPTGTEHRERVOTGKYEYITKLNINRVD 540  
 DB 541 SMKITDGAASSTFDLTNNVVRIGIELDNAGNVTKTETKIIAKLGEEDDNVFGSGTTEI 600  
 QY 541 SMKITDGAASSTFDLTNNVVRIGIELDNAGNVTKTETKIIAKLGEEDDNVFGSGTTEI 600  
 DB 601 DGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
 QY 601 DGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
 DB 661 KTEYRHSNNQHHAGYTTKDTLKAVEREICTSHNDIFKSGKENDAFNGGVDGVDITDNGDN 720  
 QY 661 KTEYRHSNNQHHAGYTTKDTLKAVEREICTSHNDIFKSGKENDAFNGGVDGVDITDNGDN 720  
 DB 721 DRLFGKGDDIILDGNGDDFIDGKGNDLLHGGKGDNDIFVHRKGDNDIITDSDGNDKLS 780  
 QY 721 DRLFGKGDDIILDGNGDDFIDGKGNDLLHGGKGDNDIFVHRKGDNDIITDSDGNDKLS 780  
 DB 781 FSDSNLKDLEFVKVHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIQG 840  
 QY 781 FSDSNLKDLEFVKVHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEEIQG 840  
 DB 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYVELLKHKNVTNSLDKLSSVSFTSSN 900  
 QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYVELLKHKNVTNSLDKLSSVSFTSSN 900  
 DB 901 DSRNLVAPTSMLDQSLSSLOFARG 926  
 QY 901 DSRNLVAPTSMLDQSLSSLOFARG 926  
 RESULT 11  
 ID US-09-124-491-6 STANDARD; PRT: 926 AA.  
 AC xxxxxx  
 DT  
 XX  
 XX  
 XX  
 DE Sequence 6, Application US/09124491  
 CC Sequence 6, Application US/09124491  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: MANN, JOHN G.  
 CC TITLE OF INVENTION: GORH-LEUKOTOXIN CHIMERAS  
 CC NUMBER OF SEQUENCES: 34  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS LLP



CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: PALO ALTO  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/09/124,491  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/694,865  
CC FILING DATE: 09-AUG-1996  
CC APPLICATION NUMBER: US 08/387,156  
CC FILING DATE: 10-FEB-1995  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960,932  
CC FILING DATE: 14-OCT-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/779,171  
CC FILING DATE: 16-OCT-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: MCCracken, THOMAS P.  
CC REGISTRATION NUMBER: 38,548  
CC REFERENCE/DOCKET NUMBER: 9001-0016.22  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415)327-3400  
CC TELEFAX: (415)327-3231  
CC INFORMATION FOR SEQ ID NO: 6:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 926 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 926 AA: 99346 MW: 4207190 CN;

Query Match 98.6%; Score 6128; DB 15; Length 926;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPKTKGAKKIIILYIPQNYQDTEQNGQLDLVKAEEELGIEVQREERNIATA 60  
QY 1 MATVIDLSPKTKGAKKIIILYIPQNYQDTEQNGQLDLVKAEEELGIEVQREERNIATA 60  
Db 61 OTSLGTIQTALGTGIVLSAPOIDKLLQKTGAGLGSASISIVONANKAKTVLSGIQS 120  
QY 61 OTSLGTIQTALGTGIVLSAPOIDKLLQKTGAGLGSASISIVONANKAKTVLSGIQS 120  
Db 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELNSLIENIANSVKTLDFEGEIOISFGSKL 180  
QY 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELNSLIENIANSVKTLDFEGEIOISFGSKL 180  
Db 181 QNKGTLGLDKLNKIGGLDKAGLDVITGLLSGATAALVLDKNAKTVKVGAGFELA 240  
QY 181 QNKGTLGLDKLNKIGGLDKAGLDVITGLLSGATAALVLDKNAKTVKVGAGFELA 240  
Db 241 NOVGNITKAVSSYILAQRVAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
QY 241 NOVGNITKAVSSYILAQRVAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
Db 301 ESYAERFKKLGVDGNLAEYORGVTIDASTANTALAAAGGVSAAAAGSVIASPTA 360  
QY 301 ESYAERFKKLGVDGNLAEYORGVTIDASTANTALAAAGGVSAAAAGSVIASPTA 360  
Db 361 LLVSGITGVISTILOYSKOAMEHVANKTHNKIVWEKNNHKNKFYNGYDARYLANLQD 420  
QY 361 LLVSGITGVISTILOYSKOAMEHVANKTHNKIVWEKNNHKNKFYNGYDARYLANLQD 420  
Db 421 NMKFLNKLQAEVIAITQQQWNNIGDLAGISRLGKLVLSGKAYVDAFEKGKHIKA 480

QY 421 NMKFLNKLQAEVIAITQQQWNNIGDLAGISRLGKLVLSGKAYVDAFEKGKHIKA 480  
Db 481 DKLVQDSANGIIDVNSGKAKTQHILFRTPLTPGTGTEHRRVQTKYIEYITKLNINRVD 540  
QY 481 DKLVQDSANGIIDVNSGKAKTQHILFRTPLTPGTGTEHRRVQTKYIEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNVVQIRIGIELDNAGNVTKTKETIIAKLGEODNVFVSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNVVQIRIGIELDNAGNVTKTKETIIAKLGEODNVFVSGTTEI 600  
Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNNQHAGYITKDTLKAVEEIIIGTSHNDIFKSGKFENDAFNGDGVDTIDGNDGN 720  
QY 661 KIEYRHSNNQHAGYITKDTLKAVEEIIIGTSHNDIFKSGKFENDAFNGDGVDTIDGNDGN 720  
Db 721 DRLFGGKDDIILDGGNGDDFDGGKGNDDLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFGGKDDIILDGGNGDDFDGGKGNDDLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780  
Db 781 FSDSNLKDITFEKVKNLVIITNSKKEVYTIQNWFEADFAKEVPNYKATKDEKIEEIIIG 840  
QY 781 FSDSNLKDITFEKVKNLVIITNSKKEVYTIQNWFEADFAKEVPNYKATKDEKIEEIIIG 840  
Db 841 NGERITSQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSASTSSN 900  
QY 841 NGERITSQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSASTSSN 900  
Db 901 DSRNVLVAPTSMLOQSLSLQFARGS 926  
QY 901 DSRNVLVAPTSMLOQSLSLQFARGS 926  
RESULT 12  
ID US-08-455-970-10 STANDARD: PRT; 943 AA.  
XX  
AC xxxxxx  
DT  
DX  
DE Sequence 10, Application US/08455970  
CC Sequence 10, Application US/08455970  
CC GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.  
CC APPLICANT: REDMOND, MARK J.  
CC APPLICANT: HUGHES, HOW P.A.  
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
CC NUMBER OF SEQUENCES: 15  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455,970  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960,932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:



CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 10:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 943 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 943 AA: 101229 MW: 4397993 CN;

Query Match	98.6%	Score 6128	DB 8	Length 943
Best Local Similarity	100.0%	Pred. No. 0.00e+00		
Matches	926	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Db	1	MATVIDLSFPKTKAKKILILIPONYQVDTGGNGLODLVKAABELGIEVOREERNIATA	60	
Qy	1	MATVIDLSFPKTKAKKILILIPONYQVDTGGNGLODLVKAABELGIEVOREERNIATA	60	
Db	61	QTSIGTTQTAIGTERGIVLSAPQIDKLLQKTAGQALGSAESIVONAKKAKTVLSG IQS	120	
Qy	61	QTSIGTTQTAIGTERGIVLSAPQIDKLLQKTAGQALGSAESIVONAKKAKTVLSG IQS	120	
Db	121	ILGSVLAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLD EFG EIQISQFGSKL	180	
Qy	121	ILGSVLAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLD EFG EIQISQFGSKL	180	
Db	181	QNIKGLGTIGDKLKNITGGLDKAGLGLDVISGLLSGATAALVLADKKNASTAKKVCAGFELA	240	
Qy	181	QNIKGLGTIGDKLKNITGGLDKAGLGLDVISGLLSGATAALVLADKKNASTAKKVCAGFELA	240	
Db	241	NOVVGNITTKAVSSYILAORVAAGLSTSGPVAALIASTVSLAISP LAFAGTADFNHAKSL	300	
Qy	241	NOVVGNITTKAVSSYILAORVAAGLSTSGPVAALIASTVSLAISP LAFAGTADFNHAKSL	300	
Db	301	ESYAERFKKLG YDGNLLA EYRQGTGT IDASVTAIN TALAAIAGGVSAAAAGSVIASPIA	360	
Qy	301	ESYAERFKKLG YDGNLLA EYRQGTGT IDASVTAIN TALAAIAGGVSAAAAGSVIASPIA	360	
Db	361	LLVSGITGVISTILQYSKQAMFEHVANKINKIVEKKNHGNYPENG YDAYLANLQD	420	
Qy	361	LLVSGITGVISTILQYSKQAMFEHVANKINKIVEKKNHGNYPENG YDAYLANLQD	420	
Db	421	NMFLLNLNKLQEAQVIAITQQOQMDNINIGDLAGISPLGKVLSGRAYDFAFEGKH IKA	480	
Qy	421	NMFLLNLNKLQEAQVIAITQQOQMDNINIGDLAGISPLGKVLSGRAYDFAFEGKH IKA	480	
Db	481	DKLVQDLSANGI IDVNSGKRAKTHILFRPLTTPGTEHREVRQTKGYEITKLINRVD	540	
Qy	481	DKLVQDLSANGI IDVNSGKRAKTHILFRPLTTPGTEHREVRQTKGYEITKLINRVD	540	
Db	541	SWKITDGAASSTEDLTNNVQRI GIELDNAGNVTKETKIIAKLGBEGDDNVFVGSCTEI	600	
Qy	541	SWKITDGAASSTEDLTNNVQRI GIELDNAGNVTKETKIIAKLGBEGDDNVFVGSCTEI	600	
Db	601	DGEGYDRVHYSRGNYCALLIDATKETEQSYTVNRVETGKALHEVYTSHTALVGNREE	660	
Qy	601	DGEGYDRVHYSRGNYGALTIDATKETEQSYTVNRVETGKALHEVYTSHTALVGNREE	660	
Db	661	KIEYRHSNNQHHAGYTKDTLKAVEELIIGTSHNDIFKGSKFNDAFNGGCGVDITDGN DGN	720	
Qy	661	KIEYRHSNNQHHAGYTKDTLKAVEELIIGTSHNDIFKGSKFNDAFNGGCGVDITDGN DGN	720	
Db	721	DRLFGGKGDDILDGNGDDDFIDGGKGNLHLHGKGDDIFVHRKGDGNDNIITDSDGNDKLS	780	
Qy	721	DRLFGGKGDDILDGNGDDDFIDGGKGNLHLHGKGDDIFVHRKGDGNDNIITDSDGNDKLS	780	
Db	781	FSDSNLKDILTFEKVKHNLVITNSKKKVTQIQQNFREADF AKEVPNYKATKDEKIEELIGQ	840	
Qy	781	FSDSNLKDILTFEKVKHNLVITNSKKKVTQIQQNFREADF AKEVPNYKATKDEKIEELIGQ	840	

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Db 841 NGERITSQVDDLLIANGKIGTQDELISKVVDNYELLKHKSNVTNSDKLISSVSAFTSSN 900
Qy 841 NGERITSQVDDLLIANGKIGTQDELISKVVDNYELLKHKSNVTNSDKLISSVSAFTSSN 900
Db 901 DSRNVLVAPTSMLDQSLSSLOFARGS 926
Qy 901 DSRNVLVAPTSMLDQSLSSLOFARGS 926
RESULT 13
ID US-07-779-171-12 STANDARD; PRT; 943 AA.
XX XXXXX
XX
XX
DT
DE
DE
XX
XX
Sequence 12, Application US/07779171
Sequence 12, Application US/07779171
GENERAL INFORMATION:
CC APPLICANT: Potter, Andrew A.
CC APPLICANT: Redmond, Mark J.
CC APPLICANT: Hughes, Huw P.A.
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
CC TITLE OF INVENTION: PASTEURELLA HEAMOLYTICA LEUKOTOXIN CHIMERAS
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morrison & Foerster
CC STREET: 545 Middlefield Road, Suite 200
CC CITY: Menlo Park
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94025
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/779,171
CC FILING DATE: 19911016
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 29310-2001600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-327-7250
CC TELEFAX: 415-327-2951
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 943 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 943 AA; 101229 MW; 4397993 CN;

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Query Match      98.6%; Score 6128; DB 3; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTGAKKIILYPQNYQYDTEGGGLQDLVKAAEELGLGVORENNIATA 60
Qy 1 MATVIDLSFPKTGAKKIILYPQNYQYDTEGGGLQDLVKAAEELGLGVORENNIATA 60

Db 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTQAGQALGSAESIVQNANKAKTVLSGIQS 120
Qy 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTQAGQALGSAESIVQNANKAKTVLSGIQS 120

Db 121 ILGSVLGAMDLDLQNNNSQHALAKAGLELTNSLIENIANSYKTLDFEFGQISQFGSKL 180

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QY 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180  
Db 181 QNTKGLGTGDKLKNKTGGDLKAGLDVTSGLLSGATAALVLADKNASTAKVKGAGFELA 240  
QY 181 QNTKGLGTGDKLKNKTGGDLKAGLDVTSGLLSGATAALVLADKNASTAKVKGAGFELA 240  
Db 241 NOVVGNTIKAVSSYIIAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKENHAKSL 300  
QY 241 NOVVGNTIKAVSSYIIAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKENHAKSL 300  
Db 301 ESYAERFKLGYDGNLLAEYQRGTTIDASVTAINATAAAGGVSAAAAGSVIASPTA 360  
QY 301 ESYAERFKLGYDGNLLAEYQRGTTIDASVTAINATAAAGGVSAAAAGSVIASPTA 360  
Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHKNKIVEWKNHGNKPNFYDARYLANLQD 420  
QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHKNKIVEWKNHGNKPNFYDARYLANLQD 420  
Db 421 NMKFLNLNKLQAEVIAITQQQWNNNGDLAGISRLGKVLGSKAYVDFAFEGKHKA 480  
QY 421 NMKFLNLNKLQAEVIAITQQQWNNNGDLAGISRLGKVLGSKAYVDFAFEGKHKA 480  
Db 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLTPTGTEHRRVQTKGYEYITKLNINRVD 540  
QY 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLTPTGTEHRRVQTKGYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNVVORIGIELDNAGNVTKTKETKIIAKLGBGDDNVFVSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNVVORIGIELDNAGNVTKTKETKIIAKLGBGDDNVFVSGTTEI 600  
Db 601 DGEQYDRVHYSRNGYALTIADATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
QY 601 DGEQYDRVHYSRNGYALTIADATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREE 660  
Db 661 KIEYRHSNNQHAGYYTKOTLKAVEREIICTSHNDIFKSGKFNDAFNGGVDITIDGNDGN 720  
QY 661 KIEYRHSNNQHAGYYTKOTLKAVEREIICTSHNDIFKSGKFNDAFNGGVDITIDGNDGN 720  
Db 721 DRLFGKGKDDILDGGGDDFDIGGKNDLLHGGKGDIDFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFGKGKDDILDGGGDDFDIGGKNDLLHGGKGDIDFVHRKGGDNDIITDSGNDKLS 780  
Db 781 FSDSNLKDILTFEKKHNLVITNSKKEKVITQWTFREADFAKEVPYKATKDEKIEEIQG 840  
QY 781 FSDSNLKDILTFEKKHNLVITNSKKEKVITQWTFREADFAKEVPYKATKDEKIEEIQG 840  
Db 841 NGERITSKQVDDLIAGKNGKITQDELSKVVDNYVELLKHKNVTNSLDKLISVSVAFTSSN 900  
QY 841 NGERITSKQVDDLIAGKNGKITQDELSKVVDNYVELLKHKNVTNSLDKLISVSVAFTSSN 900  
Db 901 DSRNVLVAPTSMLDQSLSLQFARG 926  
QY 901 DSRNVLVAPTSMLDQSLSLQFARG 926

RESULT 14

ID US-07-779-171-8 STANDARD: PRT: 951 AA.

AC xxxxxx

Sequence 8, Application US/07779171

Sequence 8, Application US/07779171

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Redmond, Mark J.

APPLICANT: Hughes, Huw P.A.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING

TITLE OF INVENTION: PASTEURILLA HEAMOLYTICA LEUKOTOXIN CHIMERAS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Morrison & Foerster  
CC STREET: 345 Middlefield Road, Suite 200  
CC CITY: Menlo Park  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94025  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/07779,171  
CC FILING DATE: 19911016  
CC CLASSIFICATION: 424  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 29310-2001600  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-327-7250  
CC TELEFAX: 415-327-2951  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 951 amino acids  
CC TYPE: AMINO ACID  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 951 AA; 102128 MW; 4463354 CN;

Query Match 98.6%; Score 6128; DB 3; Length 951;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTAGKIIILYIPQNYQYDTEQNGLQDLVKAEEELGIVQREERNIATA 60  
QY 1 MATVIDLSFPKTAGKIIILYIPQNYQYDTEQNGLQDLVKAEEELGIVQREERNIATA 60  
Db 61 QTSLGTIQTALGTGTERGIVLSAPOIDKLLQTKAGQALGSAESIVONANKAKTVLSGIQS 120  
QY 61 QTSLGTIQTALGTGTERGIVLSAPOIDKLLQTKAGQALGSAESIVONANKAKTVLSGIQS 120  
Db 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180  
QY 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180  
Db 181 QNTKGLGTGDKLKNKTGGDLKAGLDVTSGLLSGATAALVLADKNASTAKVKGAGFELA 240  
QY 181 QNTKGLGTGDKLKNKTGGDLKAGLDVTSGLLSGATAALVLADKNASTAKVKGAGFELA 240  
Db 241 NOVVGNTIKAVSSYIIAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKENHAKSL 300  
QY 241 NOVVGNTIKAVSSYIIAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKENHAKSL 300  
Db 301 ESYAERFKLGYDGNLLAEYQRGTTIDASVTAINATAAAGGVSAAAAGSVIASPTA 360  
QY 301 ESYAERFKLGYDGNLLAEYQRGTTIDASVTAINATAAAGGVSAAAAGSVIASPTA 360  
Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHKNKIVEWKNHGNKPNFYDARYLANLQD 420  
QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHKNKIVEWKNHGNKPNFYDARYLANLQD 420  
Db 421 NMKFLNLNKLQAEVIAITQQQWNNNGDLAGISRLGKVLGSKAYVDFAFEGKHKA 480  
QY 421 NMKFLNLNKLQAEVIAITQQQWNNNGDLAGISRLGKVLGSKAYVDFAFEGKHKA 480  
Db 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLTPTGTEHRRVQTKGYEYITKLNINRVD 540  
QY 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLTPTGTEHRRVQTKGYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNVVORIGIELDNAGNVTKTKETKIIAKLGBGDDNVFVSGTTEI 600  
QY 541 SWKITDGAASSTFDLTNVVORIGIELDNAGNVTKTKETKIIAKLGBGDDNVFVSGTTEI 600

QY 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGSTTEI 600  
Db 601 DGGEGYDRVHYSRGNVYKTLIDATKTEGSGSYVNRVETGKALHEVTSHTALVGNREE 660  
QY 601 DGGEGYDRVHYSRGNVYKTLIDATKTEGSGSYVNRVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNQHAGYYTKTLKAVEEIICTSHNDIFKSGKENDAFNGGVDITDGNNGN 720  
QY 661 KIEYRHSNQHAGYYTKTLKAVEEIICTSHNDIFKSGKENDAFNGGVDITDGNNGN 720  
Db 721 DRLFGKGDDIILDDGGNDGDFIDGKGNLHGGKGGDIFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFGKGDDIILDDGGNDGDFIDGKGNLHGGKGGDIFVHRKGGDNDIITDSGNDKLS 780  
Db 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEIIQ 840  
QY 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEIIQ 840  
Db 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900  
QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900  
Db 901 DSRNLVAPTSMLDQSLSLQFARG 926  
QY 901 DSRNLVAPTSMLDQSLSLQFARG 926

RESULT 15  
ID US-08-455-970-14 STANDARD; PRT; 951 AA.  
XX  
AC  
XX  
XX  
DT

Sequence 14, Application US/08455970  
Sequence 14, Application US/08455970  
GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.  
CC APPLICANT: REDMOND, MARK J.  
CC APPLICANT: HUGHES, HUW P.A.  
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
CC TITLE OF INVENTION: CHIMERAS  
CC NUMBER OF SEQUENCES: 15  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455,970  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960,932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 14:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 951 amino acids

CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 951 AA; 102128 MW; 4463354 CN;  
Query Match 98.6%; Score 6128; DB 8; Length 951;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIIATA 60  
QY 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIIATA 60  
Db 61 QTSLSGTIQTALIGLTERGIVLSAPQIDKLQTKAGCALGSAESIYQNAKAKTVLSGSIOS 120  
QY 61 QTSLSGTIQTALIGLTERGIVLSAPQIDKLQTKAGCALGSAESIYQNAKAKTVLSGSIOS 120  
Db 121 ILGSLVLAGMDLDEALQNNNSQHALAKAGLELNTSLNIENIANSVKTLDFEGEIOISQFGSKL 180  
QY 121 ILGSLVLAGMDLDEALQNNNSQHALAKAGLELNTSLNIENIANSVKTLDFEGEIOISQFGSKL 180  
Db 181 QNIKGLTIGDKLKNIGGLDKAGLDVIGLGLSGATAALVLAADKNASTAKKVGAGFELA 240  
QY 181 QNIKGLTIGDKLKNIGGLDKAGLDVIGLGLSGATAALVLAADKNASTAKKVGAGFELA 240  
Db 241 NOVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
QY 241 NOVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300  
Db 301 ESYAERFKLGYDGNLLAAYORGTGTIDASVTAINTALAAIAGGVSAAGSASPIA 360  
QY 301 ESYAERFKLGYDGNLLAAYORGTGTIDASVTAINTALAAIAGGVSAAGSASPIA 360  
Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHKNKIVWEKNHGNKYNFENGVDARYLANLOD 420  
QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHKNKIVWEKNHGNKYNFENGVDARYLANLOD 420  
Db 421 NMKFLNLNKLQAEVRIATITQQOWDNNIGDLAGISRLGEKVLGKAYVDAFEKGHIKA 480  
QY 421 NMKFLNLNKLQAEVRIATITQQOWDNNIGDLAGISRLGEKVLGKAYVDAFEKGHIKA 480  
Db 481 DKLVLDSANGIIDVSNKSKAKTOHILFPTPLLTPTGTEHREVRVOTGKYEYITKLNINRVD 540  
QY 481 DKLVLDSANGIIDVSNKSKAKTOHILFPTPLLTPTGTEHREVRVOTGKYEYITKLNINRVD 540  
Db 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGSTTEI 600  
QY 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNVFVSGSTTEI 600  
Db 601 DGGEGYDRVHYSRGNVYKTLIDATKTEGSGSYVNRVETGKALHEVTSHTALVGNREE 660  
QY 601 DGGEGYDRVHYSRGNVYKTLIDATKTEGSGSYVNRVETGKALHEVTSHTALVGNREE 660  
Db 661 KIEYRHSNQHAGYYTKTLKAVEEIICTSHNDIFKSGKENDAFNGGVDITDGNNGN 720  
QY 661 KIEYRHSNQHAGYYTKTLKAVEEIICTSHNDIFKSGKENDAFNGGVDITDGNNGN 720  
Db 721 DRLFGKGDDIILDDGGNDGDFIDGKGNLHGGKGGDIFVHRKGGDNDIITDSGNDKLS 780  
QY 721 DRLFGKGDDIILDDGGNDGDFIDGKGNLHGGKGGDIFVHRKGGDNDIITDSGNDKLS 780  
Db 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEIIQ 840  
QY 781 FSDSNLKDITFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNYKATKDEKIEIIQ 840  
Db 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900  
QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900  
Db 901 DSRNLVAPTSMLDQSLSLQFARG 926  
QY 901 DSRNLVAPTSMLDQSLSLQFARG 926

Search completed: Wed Dec 9 19:35:47 1998  
Job time : 252 secs.

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